

| | | | | | |
|----|-------|-------|-----|----|----------|
| 12 | 260 | 100.0 | 197 | 21 | AA95922 |
| 13 | 260 | 100.0 | 203 | 17 | AAW06107 |
| 14 | 260 | 100.0 | 203 | 17 | AAW06108 |
| 15 | 260 | 100.0 | 373 | 17 | AAW06103 |
| 16 | 260 | 100.0 | 375 | 17 | AAW06104 |
| 17 | 260 | 100.0 | 385 | 17 | AAW06102 |
| 18 | 260 | 100.0 | 492 | 17 | AAW06105 |
| 19 | 252 | 96.9 | 170 | 14 | AA835440 |
| 20 | 234 | 90.0 | 168 | 11 | AA804717 |
| 21 | 234 | 90.0 | 168 | 11 | AA848594 |
| 22 | 234 | 90.0 | 170 | 14 | AA830736 |
| 23 | 221.5 | 85.2 | 169 | 15 | AA848593 |
| 24 | 220.5 | 84.8 | 170 | 11 | AA802226 |
| 25 | 220.5 | 84.8 | 170 | 14 | AA830735 |
| 26 | 220.5 | 84.8 | 170 | 15 | AA845947 |
| 27 | 220.5 | 84.8 | 170 | 17 | AA86422 |
| 28 | 220.5 | 84.8 | 170 | 19 | AA857236 |
| 29 | 220.5 | 84.8 | 170 | 21 | AA58368 |
| 30 | 220 | 84.6 | 41 | 20 | AA504044 |
| 31 | 201.5 | 77.5 | 167 | 15 | AA848595 |
| 32 | 198 | 76.2 | 40 | 21 | AA812612 |
| 33 | 198 | 76.2 | 40 | 21 | AA85559 |
| 34 | 197.5 | 76.0 | 127 | 15 | AA848596 |
| 35 | 194 | 74.6 | 39 | 21 | AA85561 |
| 36 | 142.5 | 54.8 | 103 | 22 | AAU02049 |
| 37 | 142.5 | 54.8 | 273 | 22 | AAU02052 |
| 38 | 142.5 | 54.8 | 342 | 22 | AAU02053 |
| 39 | 139 | 53.5 | 25 | 17 | AA895342 |
| 40 | 139 | 53.5 | 25 | 18 | AA843948 |
| 41 | 135 | 51.9 | 24 | 15 | AA849336 |
| 42 | 135 | 51.9 | 24 | 16 | AA874158 |
| 43 | 135 | 51.9 | 24 | 19 | AAW54719 |
| 44 | 135 | 51.9 | 24 | 22 | AAU06294 |
| 45 | 135 | 51.9 | 24 | 22 | AA84534 |

Human myelin bindi
Foetal myelin basi
Foetal myelin basi
MP4 chimera (MBP21
MP4 chimera (delta
MP3 chimera (MBP21
MMOGP4 chimera (MB
Human basic myelin
Empirically determ
Rabbit myelin basi
Human MBP. Synthe
Cattle myelin basi
Myelin basic prote
Bovine MBP. Synth
Myelin basic prote
Myelin basic prote
Myelin basic prote
Mammalian generi
Human myelin basic
Myelin basic prote
Human myelin basic
Human MBP peptide
Rat myelin basic p
Human MBP peptide
Synthetic human ta
Synthetic human mu
Human myelin basic
MBP-2.5 (80-104)
Human myelin basic
Antigenic peptide
Peptide from Myell
Human Leukocyte An
Human leukocyte an

12 260 100.0 197 21 AA95922
13 260 100.0 203 17 AAW06107
14 260 100.0 203 17 AAW06108
15 260 100.0 373 17 AAW06103
16 260 100.0 375 17 AAW06104
17 260 100.0 385 17 AAW06102
18 260 100.0 492 17 AAW06105
19 252 96.9 170 14 AA835440
20 234 90.0 168 11 AA804717
21 234 90.0 168 11 AA848594
22 234 90.0 170 14 AA830736
23 221.5 85.2 169 15 AA848593
24 220.5 84.8 170 11 AA802226
25 220.5 84.8 170 14 AA830735
26 220.5 84.8 170 15 AA845947
27 220.5 84.8 170 17 AA86422
28 220.5 84.8 170 19 AA857236
29 220.5 84.8 170 21 AA58368
30 220 84.6 41 20 AA504044
31 201.5 77.5 167 15 AA848595
32 198 76.2 40 21 AA812612
33 198 76.2 40 21 AA85559
34 197.5 76.0 127 15 AA848596
35 194 74.6 39 21 AA85561
36 142.5 54.8 103 22 AAU02049
37 142.5 54.8 273 22 AAU02052
38 142.5 54.8 342 22 AAU02053
39 139 53.5 25 17 AA895342
40 139 53.5 25 18 AA843948
41 135 51.9 24 15 AA849336
42 135 51.9 24 16 AA874158
43 135 51.9 24 19 AAW54719
44 135 51.9 24 22 AAU06294
45 135 51.9 24 22 AA84534

Human myelin bindi
Foetal myelin basi
Foetal myelin basi
MP4 chimera (MBP21
MP4 chimera (delta
MP3 chimera (MBP21
MMOGP4 chimera (MB
Human basic myelin
Empirically determ
Rabbit myelin basi
Human MBP. Synthe
Cattle myelin basi
Myelin basic prote
Bovine MBP. Synth
Myelin basic prote
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Myelin basic prote
Mammalian generi
Human myelin basic
Myelin basic prote
Human myelin basic
Human MBP peptide
Rat myelin basic p
Human MBP peptide
Synthetic human ta
Synthetic human mu
Human myelin basic
MBP-2.5 (80-104)
Human myelin basic
Antigenic peptide
Peptide from Myell
Human Leukocyte An
Human leukocyte an

ALIGNMENTS

| | |
|----------|--|
| RESULT | 1 |
| AAW72360 | |
| ID | AAW72360 standard; peptide; 46 AA. |
| XX | |
| AC | AAW72360; |
| XX | |
| DT | 16-DEC-1998 (first entry) |
| XX | |
| DE | Human myelin basic protein fragment. |
| XX | |
| KW | Human; myelin basic protein; MBP; multiple sclerosis; anti-MBP; MS. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO9845327-A1. |
| XX | |
| PD | 15-OCT-1998. |
| XX | |
| PF | 03-APR-1998; 98WO-CA00290. |
| XX | |
| PR | 04-APR-1997; 97CA-2201841. |
| XX | |
| PA | (DYAL-) UNIV ALBERTA. |
| XX | |
| PI | Catz I, Warren KG; |
| XX | |
| DR | WPI; 1998-568336/48. |
| XX | |
| PT | Peptide and its derivatives for treatment of multiple sclerosis - is |
| XX | |
| PS | capable of neutralising or modulating production of anti-myelin |
| XX | |
| PS | basic protein |
| XX | |
| PS | Disclosure; Page 15; 75pp; English. |
| XX | |

Human myelin bindi
Foetal myelin basi
Foetal myelin basi
MP4 chimera (MBP21
MP4 chimera (delta
MP3 chimera (MBP21
MMOGP4 chimera (MB
Human basic myelin
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Rabbit myelin basi
Human MBP. Synthe
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Bovine MBP. Synth
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Mammalian generi
Human myelin basic
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Human MBP peptide
Rat myelin basic p
Human MBP peptide
Synthetic human ta
Synthetic human mu
Human myelin basic
MBP-2.5 (80-104)
Human myelin basic
Antigenic peptide
Peptide from Myell
Human Leukocyte An
Human leukocyte an

12 260 100.0 197 21 AA95922
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19 252 96.9 170 14 AA835440
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21 234 90.0 168 11 AA848594
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23 221.5 85.2 169 15 AA848593
24 220.5 84.8 170 11 AA802226
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27 220.5 84.8 170 17 AA86422
28 220.5 84.8 170 19 AA857236
29 220.5 84.8 170 21 AA58368
30 220 84.6 41 20 AA504044
31 201.5 77.5 167 15 AA848595
32 198 76.2 40 21 AA812612
33 198 76.2 40 21 AA85559
34 197.5 76.0 127 15 AA848596
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36 142.5 54.8 103 22 AAU02049
37 142.5 54.8 273 22 AAU02052
38 142.5 54.8 342 22 AAU02053
39 139 53.5 25 17 AA895342
40 139 53.5 25 18 AA843948
41 135 51.9 24 15 AA849336
42 135 51.9 24 16 AA874158
43 135 51.9 24 19 AAW54719
44 135 51.9 24 22 AAU06294
45 135 51.9 24 22 AA84534

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Foetal myelin basi
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MP4 chimera (delta
MP3 chimera (MBP21
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Human MBP peptide
Rat myelin basic p
Human MBP peptide
Synthetic human ta
Synthetic human mu
Human myelin basic
MBP-2.5 (80-104)
Human myelin basic
Antigenic peptide
Peptide from Myell
Human Leukocyte An
Human leukocyte an

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 260 | 100.0 | 46 | 19 | AAW72360 |
| 2 | 260 | 100.0 | 170 | 15 | AA848592 |
| 3 | 260 | 100.0 | 170 | 17 | AA895406 |
| 4 | 260 | 100.0 | 171 | 17 | AA897627 |
| 5 | 260 | 100.0 | 171 | 17 | AA899580 |
| 6 | 260 | 100.0 | 171 | 20 | AA827284 |
| 7 | 260 | 100.0 | 171 | 21 | AA819513 |
| 8 | 260 | 100.0 | 171 | 21 | AA869394 |
| 9 | 260 | 100.0 | 171 | 21 | AA844234 |
| 10 | 260 | 100.0 | 186 | 21 | AA857090 |
| 11 | 260 | 100.0 | 197 | 17 | AAW00399 |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CC The present sequence represents a myelin basic protein (MBP) protein
 CC fragment used to produce MBP peptides. MBP peptides are capable of
 CC neutralising or modulating the production of anti-myelin basic protein.
 CC The present invention also describes a method for treating multiple
 CC sclerosis (MS). The method comprises administering to the patient an
 CC MBP peptide of the formula: R1-Val-His-Phe-Phe-Lys-Asn-Ile-R2 where R1,
 CC R2 = H, OH, or an amino acid residue and a polypeptide residue,
 CC provided that R1 and R2 are not both H or OH at the same time.
 XX
 SQ Sequence 46 AA;

Query Match 100.0%; Score 260; DB 19; Length 46;
 Best Local Similarity 100.0%; Pred. No. 7.4e-27;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGSIPQKSHGRGTQDENPVVHFFKNIVTPTPPPSQKG 46
 |||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 hhpatahygsipqkshgrtqdenpvvhffknivtptpppsqkg 46

RESULT 2
 AAR48592
 ID AAR48592 standard; protein; 170 AA.

XX AC AAR48592;

XX DT 31-JUL-1994 (first entry)

XX DE Human myelin basic protein.

XX KW Proteolipid protein; myelin basic protein; retrovirus;
 KW neurological disease; by-stander antigen; TGF-beta;
 KW transforming growth factor-beta; T-cell; T-lymphocyte;
 KW myelopathy; paraparesis; human immunodeficiency virus type 1.

XX OS Homo sapiens.

XX PN WO9404121-A.

XX PD 03-MAR-1994.

XX PF 17-AUG-1993; 93WO-US07786.

XX PR 17-AUG-1992; 92US-0931217.

XX PA (AUTO-) AUTOIMMUNE INC.

XX PI Hafler DA, Weiner HL;

XX WPI; 1994-082786/10.

XX PT Treating retroviral associated neurological disease - by admin.
 PT of by-stander antigen, causing release of transforming growth
 PT factor beta from suppressor T cells

XX PS Disclosure; Page 49; 64pp; English.

XX CC Myelin basic proteins (sequences AAR48592-96) and cattle proteolipid
 CC protein (AAR48592) elicit the release of TGF-beta from suppressor T-
 CC cells and target the T-cells to neural tissue under cytotoxic
 CC attack, thereby reducing neurological disease, e.g. HTLV-1
 CC associated myelopathy, tropical spastic paraparesis and HIV
 CC infection.

XX SQ Sequence 170 AA;

Query Match 100.0%; Score 260; DB 15; Length 170;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGSIPQKSHGRGTQDENPVVHFFKNIVTPTPPPSQKG 46

Db 61 hhpatahygsipqkshgrtqdenpvvhffknivtptpppsqkg 106

RESULT 3

ID AAR95406

XX AAR95406 standard; Protein; 170 AA.

XX AC AAR95406;

XX DT 16-DEC-1996 (first entry)

XX DE Myelin oligodendrocyte protein.

XX KW Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.

XX OS Homo sapiens.

XX PN WO9612737-A2.

XX PD 02-MAY-1996.

XX PF 25-OCT-1995; 95WO-US13682.

XX PR 15-MAR-1995; 95US-0404228.

XX PR 25-OCT-1994; 94US-0328224.

XX PR 25-OCT-1995; 95ZA-0009033.

XX PA (IMMU-) IMMULOGIC PHARM CORP.

XX PI Devaux B, Franzen H, Geftter M, Hsu D, Pallard X;

XX PI Rothbard J, Samson M, Shi J, Smilek D;

XX WPI; 1996-230552/23.

XX PT Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.

XX PS Example 9; Fig 1; 91pp; English.

XX CC This sequence represents the human myelin oligodendrocyte protein (MOG).
 CC Immunisation with MOG (or the peptide fragments shown in
 CC AAR95375-R95385) can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for treating
 CC MS in a mammal. The composition acts to down regulate the autoimmune
 CC response, and may be administered in an amount sufficient to prevent the
 CC onset of symptoms of MS. The compositions may also be used to treat
 CC advanced stage MS, especially relapsing-remitting MS, chronic progressive
 CC MS or benign MS. These peptides may also be used in the treatment of
 CC other diseases involving myelin autoantigens, including diabetes, Graves
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,
 CC thyroiditis, and rheumatoid arthritis. Peptides derived from other
 CC myelin autoantigens, such as myelin basic protein (MBP, see
 CC AAR95334-R95374), proteolipid protein (PLP), and myelin associated
 CC glycoprotein (MAG) can be used as alternatives to the MOG peptides in
 CC these compositions.

XX SQ Sequence 170 AA;

Query Match 100.0%; Score 260; DB 17; Length 170;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTRTPPPSQGK 46
 |||||
 Db 61 hhpatahygslpqlkshgrtqdenpvvhffknivtrtpppsqgk 106

RESULT 4

AAR97627 4
 ID AAR97627 standard; Protein; 171 AA.

XX
 AC AAR97627;

XX 09-NOV-1996 (first entry)

XX Human myelin basic protein.

XX Myelin basic protein; MBP; multiple sclerosis; MS; treatment;

XX prevention; analogue.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 86..99

FT /label= Claimed peptide region.

XX WO9616085-A1.

XX 30-MAY-1996.

XX 16-NOV-1995; 95WO-US14402.

XX 18-NOV-1994; 94US-0342078.

XX (NEUR-) NEUROCRINE BIOSCIENCES INC.

PA (STRD) UNIV STANFORD MEDICAL CENT.

XX Conlon PJ, Gaur A, Ling N, Steinman L;

XX WPI; 1996-268534/27.

XX N-PSDB; AAT30269.

XX Peptide analogue of human myelin basic protein - has Lysine 91
 replaced by another amino acid, useful to treat multiple sclerosis

PS Claim 1: Figure 1: 30pp; English.

XX A peptide analogue comprising amino acids 87-99 of human myelin
 basic protein (MBP), where Lys91 is substituted for another amino
 acid can be used to treat and prevent multiple sclerosis. The
 CC peptide analogue is administered at a dosage range of 5-50 mg/kg.

XX Sequence 171 AA;

Query Match 100.0%; Score 260; DB 17; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTRTPPPSQGK 46
 |||||
 Db 62 hhpatahygslpqlkshgrtqdenpvvhffknivtrtpppsqgk 107

RESULT 5

AAR99580

ID AAR99580 standard; Protein; 171 AA.

XX AAR99580;

XX 07-NOV-1996 (first entry)

XX Human myelin basic protein (MBP).

KW Myelin basic protein; MBP; multiple sclerosis; MS; competition;
 KW inhibition; major histocompatibility complex; MHC; thymocyte; T cell;
 XX experimental allergic encephalomyelitis; EAE; analogue.

OS Homo sapiens.

XX WO9616086-A1.

XX 30-MAY-1996.

XX 16-NOV-1995; 95WO-US14403.

XX 18-NOV-1994; 94US-0342408.

XX (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX Conlon PJ, Gaur A, Ling N, Steinman L;

XX WPI; 1996-268535/27.

XX N-PSDB; AAT32561.

XX Peptide analogues of human myelin basic protein - useful for
 treatment of multiple sclerosis

XX Disclosure; Figure 1; 61pp; English.

XX Peptide analogues comprising at least seven amino acids from
 residues 86-99 of human myelin basic protein (MBP), can be used to
 treat multiple sclerosis by competing for the binding of native MBP
 CC peptide to MHC and by not causing proliferation of an MBP reactive T-
 CC cell line. The peptide analogues also inhibit the induction of
 CC experimental allergic encephalomyelitis (EAE) by MBP in rodents.
 CC The peptide analogues have a reduced susceptibility to proteolysis
 CC in vivo.

XX Sequence 171 AA;

Query Match 100.0%; Score 260; DB 17; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTRTPPPSQGK 46
 |||||
 Db 62 hhpatahygslpqlkshgrtqdenpvvhffknivtrtpppsqgk 107

RESULT 6

AAV27284

ID AAV27284 standard; Protein; 171 AA.

XX AAV27284;

XX 29-OCT-1999 (first entry)

XX Human myelin basic protein (MBP).

KW Myelin basic protein; MBP; peptide analogue; MHC; multiple sclerosis;
 KW T-cell reactivity; major histocompatibility complex; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 86..99

FT /note= "peptide analogues of the invention comprise
 at least seven consecutive amino acid residues
 from this region"

FT Misc-difference 97

FT /note= "the L-Arg at this position can be altered to
 a D-amino acid and especially to a D-Ala to
 construct the peptide analogues (see claims 2
 and 3"

PN US5948764-A.
 XX
 PD 07-SEP-1999.
 XX
 PF 09-JAN-1997; 97US-0781122.
 XX
 PR 09-JAN-1997; 97US-0781122.
 XX
 PR 09-MAR-1995; 95US-0402992.
 XX
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 XX
 PI Conlon PJ, Gaur A, Ling N;
 XX
 DR WPI; 1999-517966/43.
 DR N-PSDB; AA200399.
 XX
 PT Human myelin basic protein analogues useful for the treatment of
 PT multiple sclerosis
 PS Disclosure; Fig 1; 35pp; English.
 XX
 CC The invention provides human myelin basic protein (MBP) analogues. The
 CC analogues, comprise a sequence of 7 or more consecutive amino acids
 CC taken from between residues 86 to 99 of the native human MBP amino acid
 CC sequence (AA27284). The analogues include residue 97 of the human MBP
 CC sequence, however, the L-arginine at position 97 is altered to a D-amino
 CC acid. The peptide analogues may be used for treating multiple sclerosis.
 CC Multiple sclerosis may be caused by an autoimmune reaction involving
 CC T-cells which have lost their 'self-tolerance' and attack normal tissue.
 CC Therefore, T-cell reactivity to human MBP may be a major cause of the
 CC development of MS. The T-cells recognize and bind to an epitope of human
 CC MBP between amino acids 86 to 106 of the sequence. The peptide analogues
 CC (MHC) on the T-cells than human MBP and therefore interfere with the
 CC reactivity of T-cells against human MBP. Administration of the analogues
 CC may prevent future, repeated attacks of multiple sclerosis without any
 CC side effects after long-term use (such as malignancies, toxic hepatitis
 CC and immunocompromising the patient). The present sequence represents a
 CC human MBP sequence.
 XX
 SQ Sequence 171 AA;
 Query Match 100.0%; Score 260; DB 20; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFKNIVTPTPPSQGKG 46
 DB 62 hhpatahyglpqlkshgrtqdenpvvvhfkniivtrtpptpsqgkg 107
 RESULT 7
 AAB19513
 ID AAB19513 standard; Protein; 171 AA.
 AC AAB19513;
 XX
 DT 09-JAN-2001 (first entry)
 XX
 DE Human myelin basic protein.
 XX
 KW Myelin basic protein; human; autoimmune disease; autoantigen;
 KW demyelinating disease; experimental autoimmune encephalitis;
 KW multiple sclerosis; antinflammatory; DNA vaccination; vaccine;
 KW T cell; pro-inflammatory response.
 XX
 OS Homo sapiens.
 XX
 PN WO200053019-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-JAN-1997; 97US-0781122.
 XX
 PR 09-MAR-1995; 95US-0402992.
 XX
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 XX
 PI Conlon PJ, Gaur A, Ling N;
 XX
 DR WPI; 1999-517966/43.
 DR N-PSDB; AA200399.
 XX
 PT Human myelin basic protein analogues useful for the treatment of
 PT multiple sclerosis
 PS Disclosure; Fig 1; 35pp; English.
 XX
 CC The invention provides human myelin basic protein (MBP) analogues. The
 CC analogues, comprise a sequence of 7 or more consecutive amino acids
 CC taken from between residues 86 to 99 of the native human MBP amino acid
 CC sequence (AA27284). The analogues include residue 97 of the human MBP
 CC sequence, however, the L-arginine at position 97 is altered to a D-amino
 CC acid. The peptide analogues may be used for treating multiple sclerosis.
 CC Multiple sclerosis may be caused by an autoimmune reaction involving
 CC T-cells which have lost their 'self-tolerance' and attack normal tissue.
 CC Therefore, T-cell reactivity to human MBP may be a major cause of the
 CC development of MS. The T-cells recognize and bind to an epitope of human
 CC MBP between amino acids 86 to 106 of the sequence. The peptide analogues
 CC (MHC) on the T-cells than human MBP and therefore interfere with the
 CC reactivity of T-cells against human MBP. Administration of the analogues
 CC may prevent future, repeated attacks of multiple sclerosis without any
 CC side effects after long-term use (such as malignancies, toxic hepatitis
 CC and immunocompromising the patient). The present sequence represents a
 CC human MBP sequence.
 XX
 SQ Sequence 171 AA;
 Query Match 100.0%; Score 260; DB 21; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFKNIVTPTPPSQGKG 46
 DB 62 hhpatahyglpqlkshgrtqdenpvvvhfkniivtrtpptpsqgkg 107
 RESULT 8
 AAY69394
 ID AAY69394 standard; Protein; 171 AA.
 XX
 AC AAY69394;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Amino acid sequence of a human myelin basic protein.
 XX
 KW Human; myelin basic protein; oligodendroglial cell; Th2 immune response;
 KW Th2-type cytokine; analogue; multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200011027-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 19-AUG-1999; 99WO-US19033.
 XX
 PR 20-AUG-1998; 98US-0137759.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 XX

PI Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;
 XX WPI; 2000-224661/19.
 DR N-PSDB; AA261594.
 XX
 XX Inducing a Th2 immune response and a persistent systemic immune
 PT response to myelin basic protein, MBP, or a peptide analog of MBP for
 PT use in treating multiple sclerosis, by administering compositions
 PT comprising peptide analogs of MBP -
 XX
 XX Disclosure; Fig 1; 112pp; English.
 PS
 XX The present sequence represents a human myelin basic protein. Myelin
 CC basic protein is found in the cytoplasm of human oligodendroglial
 CC cells. Peptide analogues of myelin basic protein are administered to
 CC a patient in need to induce a Th2 immune response (i.e. production
 CC of T cells producing one or more Th2-type cytokines) and/or a
 CC persistent systemic immune response to myelin basic protein. These
 CC peptide analogues are at least seven amino acids long, derived from
 CC residues 83-99 of human myelin basic protein and altered from the
 CC native sequence at least at positions 91, 95 or 97. The peptide
 CC analogs are especially useful in the treatment of multiple sclerosis.
 CC
 XX Sequence 171 AA;
 SQ

Query Match 100.0%; Score 260; DB 21; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHVGSIPQKSHGRQTQDENPVVHFKNIVTPRTPPSQKG 46
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 62 hhparytgysslpqkshgrtqdenpvvfhfkniivtrtpppsqqg 107

RESULT 9
 AAY44234
 ID AAY44234 standard; Protein; 171 AA.
 XX
 AC AAY44234;
 XX
 DT 21-FEB-2000 (first entry)
 XX
 DE Human myelin basic protein.
 XX
 KW Human; myelin basic protein; MBP; NS-specific antigen;
 KW nervous system-specific antigen; T cell; peripheral nervous system; PNS;
 KW central nervous system; CNS; nerve regeneration; neuronal degeneration;
 KW spinal cord injury; blunt trauma; penetrating trauma; senile dementia;
 KW ischaemic stroke; diabetic neuropathy; glaucoma; haemorrhagic stroke;
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
 KW amyotrophic lateral sclerosis; ALS; treatment.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT Peptide
 FT 11..30
 FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"
 FT 51..70
 FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"
 FT 91..110
 FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"
 FT 131..150
 FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"
 FT 151..170

FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"
 XX WO9960021-A2.
 XX
 XX 25-NOV-1999.
 XX
 XX 19-MAY-1999; 99WO-US10953.
 XX
 XX 19-MAY-1998; 98IL-0124550.
 XX 21-JUL-1998; 98WO-US14715.
 XX 22-DEC-1998; 98US-0218277.
 XX (VEDA) YEDA RES & DEV CO LTD.
 XX (MCIN/) MCINNIS P A.
 XX
 XX Eisenbach-Schwartz M, Cohen IR, Beserman P, Mosonogo A, Moalem G;
 PI WPI; 2000-072430/06.
 XX N-PSDB; AA229197.
 DR
 XX New compositions useful to treat nervous system injury or disease e.g.
 PT traumatic injury, Alzheimer's disease etc.
 PT
 XX Claim 9; Fig 21; 92pp; English.
 PS
 XX The present sequence is a human myelin basic protein
 CC which is a nervous system-specific antigen. The antigen or peptides
 CC derived from it activate T cells in vivo. The present sequence is
 CC used to promote nerve regeneration or to prevent or inhibit neuronal
 CC degeneration caused by injury or diseases of nerves within the CNS or
 CC PNS. Such injury includes spinal cord injury, blunt trauma, penetrating
 CC trauma, haemorrhagic stroke or ischaemic stroke, whilst diseases include
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis,
 CC etc.
 XX Sequence 171 AA;
 SQ

Query Match 100.0%; Score 260; DB 21; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3.2e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHVGSIPQKSHGRQTQDENPVVHFKNIVTPRTPPSQKG 46
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 62 hhparytgysslpqkshgrtqdenpvvfhfkniivtrtpppsqqg 107

RESULT 10
 AAY57090
 ID AAY57090 standard; Protein; 186 AA.
 XX
 AC AAY57090;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Human myelin basic protein fragment.
 XX
 KW Neglected target tissue antigen; NTA; autoimmunity; autoimmune response;
 KW immunotherapeutic agent; insulin dependent diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
 KW uveoretinitis; inflammatory response.
 XX
 OS Homo sapiens.
 XX
 PN WO9956763-A1.
 XX
 PD 11-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-US10250.
 XX

| | | |
|----|--|---------------|
| PR | 07-MAY-1998; | 98US-0084636. |
| XX | (REGC) UNIV CALIFORNIA. | |
| XX | Kaufman DL, Tian J, Olcott A; | |
| PI | WPI: 2000-052905/04. | |
| DR | Administration of neglected target tissue antigens to modulate immune | |
| PT | responses - | |
| XX | Disclosure; Page 33; 79pp; English. | |
| XX | Amino acid sequences AAY57063-Y57091 are examples of neglected target | |
| CC | tissue antigens NTAs. NTAs are antigens (whole antigens or fragments) | |
| CC | not involved in autoimmunity. These peptides and proteins are used in | |
| CC | the method of the invention which involves administering an NTA as an | |
| CC | antigen based immunotherapeutic agent, to a host afflicted with an | |
| CC | autoimmune response associated with an autoimmune disease. The | |
| CC | immunotherapeutic agent is used to treat autoimmune diseases such as | |
| CC | insulin dependent diabetes mellitus, multiple sclerosis, autoimmune | |
| CC | thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal | |
| CC | inflammatory immune responses. The NTA induces regulatory tolerance by | |
| CC | elicitation of regulatory T cells among T cells recognizing the NTA but | |
| CC | not participating in the immune response. The NTA is capable of | |
| CC | recognition by substantial populations of uncommitted T cells which can | |
| CC | be primed, or biased, towards regulatory responses to provide effective | |
| CC | treatment. The NTA are effective in regulating undesirable immune | |
| CC | responses even when target determinants used as agents promoting | |
| CC | tolerance agents have failed to induce an effective regulatory T cell | |
| CC | response. NTAs as agents promoting tolerance are anticipated to be safer | |
| CC | than use of target determinants. | |
| XX | Sequence 186 AA: | |
| XX | SQ | |

```

Query Match      100.0%; Score 260; DB 21; Length 186;
Best Local Similarity 100.0%; Pred. No. 3.5e-26;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHPARTAHYGLPKQSGRTQDENPVVHFFKNIVTRTPPSSCKG 46
Db 88 hhp-artahygs.lpkqsgqrtqdenpvvhffknivtrtppsack 133

```

| | |
|----------|--|
| RESULT | ll |
| AAW00399 | |
| ID | AAW00399 standard; Protein; 197 AA. |
| XX | |
| XX | AAW00399; |
| DT | 01-FEB-1997 (first entry) |
| DD | |
| XX | Human myelin basic protein (foetal isoform). |
| DE | |
| XX | |
| KW | Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP; |
| KW | multiple sclerosis; autoimmune disease; diagnosis; therapy; |
| KW | T-lymphocyte; T-cell; anergy; apoptosis. |
| OS | Homo sapiens. |
| XX | |
| PH | Key |
| FT | Region |
| FT | 60..85 |
| FT | /label= X2 |
| FT | /note= "exon 2-encoded region" |
| FT | Misc-difference 81 |
| FT | /note= "Cys-81 may be replaced by any standard amino acid. sep. an uncharged amino acid of mol.wt. below about 150, partic. Ser, in constructs of the invention" |
| PN | WO9634622-A1. |
| XX | |

| | | | |
|----|----|---|--|
| PD | | 07-NOV-1996. | |
| XX | FF | 22-APR-1996; 96WO-US05611. | |
| XX | PR | | |
| XX | PR | 07-JUN-1995; 95US-0482114. | |
| PR | PR | 02-MAY-1995; 95US-0431644. | |
| PR | PR | 02-MAY-1995; 95US-0431648. | |
| XX | PA | (ALEX-) ALEXION PHARM INC. | |
| XX | PA | (USSH) US DEPT HEALTH & HUMAN SERVICES. | |
| PI | PI | Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP; | |
| PI | PI | Nye SH, Pelfrey CM, Squinto SP, Wilkins JA; | |
| DR | DR | WPI; 1996-505898/50. | |
| DR | DR | N-PSDB; AAT41889. | |
| XX | PT | New human myelin basic protein and proteolipid protein variant(s) - | |
| PT | PT | used in the assessment, diagnosis and treatment of multiple | |
| PT | PT | sclerosis | |
| XX | PS | Claim 1: Page 79-80; 156pp; English. | |
| XX | CC | The native human 21.5 kDa foetal isoform (AAW00399) of myelin basic | |
| CC | CC | protein, MBP-X2Cys81, includes an exon 2-encoded region [X2] that | |
| CC | CC | may contain an epitope involved in the pathogenesis of multiple | |
| CC | CC | sclerosis (MS); the X2 region is not found in the MBP of healthy | |
| CC | CC | adults. Recombinant MBP-X2, or variants modified to improve | |
| CC | CC | bacterial expression (see also AAW06107), can be produced in a | |
| CC | CC | large scale in bacterial hosts. They are useful for assaying | |
| CC | CC | T-cells for responsiveness to MBP epitopes and can be used as | |
| CC | CC | therapeutic agents that act by inducing T-cell responses, | |
| CC | CC | including anergy and apoptosis, as a means of treating MS. | |
| XX | XX | Sequence 197 AA: | |
| SQ | SQ | | |

| | Query Match | 100.0% | Score 260; | DB 17; | Length 197; |
|----|-----------------------|---|--------------------|-----------|-------------|
| | Best-Local Similarity | 100.0% | Pred. No. 3.7e-26; | | |
| | Matches 46; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | HHPARTAHYGLSPKSGRGTQDENPWHVFKNIVTRTPPSSQKG | 46 | | |
| Db | 88 | hhpartahyglspksggrgtqdenpvhfknlvtrtpposgqkq | 133 | | |

| | | |
|---------|---|--|
| RESULT | 12 | |
| AA95922 | | |
| ID | AA95922 standard; Protein; 197 AA. | |
| XX | | |
| XX | AA95922; | |
| XX | | |
| XX | 20-NOV-2000 (first entry) | |
| DT | | |
| DE | Human myelin binding protein Delta II. | |
| XX | | |
| XX | Myelin binding protein; MBP; human; GPBP; | |
| KW | goodpasture antigen binding protein; autoimmune disease; apoptosis; | |
| XX | cancer; tumour; therapy. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200050607-A2. | |
| XX | | |
| PD | 31-AUG-2000. | |
| XX | | |
| PF | 24-FEB-2000; 2000WO-IB00324. | |
| XX | | |
| PR | 24-FEB-1999; 99US-0121483. | |
| XX | | |
| PA | (SAUS/) SAUS J. | |
| XX | | |
| PI | Saus J. | |

XX WPI: 2000-572094/53.
 DR N-PSDB; AAA50371.
 XX
 PT Novel Goodpasture antigen binding proteins useful for diagnosing and
 XX treating autoimmune disorders, tumor, and preventing cell apoptosis -
 XX
 PS Claim 36; Page 157; 158pp; English.
 XX
 CC The present sequence is that of human myelin binding protein (MBP)
 CC Delta II, i.e. an alternative form of human MBP resulting from
 CC splicing out of exon II. The protein was recombinantly expressed in
 CC Pichia pastoris cells. The invention relates to novel Goodpasture
 CC antigen binding proteins (GPBs), see AAY95900-11), which bind to and
 CC phosphorylate the unique N-terminal region of human GP, and which
 CC are highly expressed in several autoimmune conditions. Claimed
 CC methods for treating an autoimmune disorder, cell apoptosis or a
 CC tumour involve modifying the expression or activity of GPBP,
 CC especially using a MBP protein or a nucleic acid sequence encoding
 CC it.
 XX Sequence 197 AA;
 SQ
 Query Match 100.0%; Score 260; DB 21; Length 197;
 Best Local Similarity 100.0%; Pred. No. 3.7e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHPARTAHYGSILPOKSHGRTOEDNPVHFFKNIVTPTPPSQGKG 46
 Db 88 hhpatahygsilpqkshgrtqdenpvvhffknivtprtppsqgkg 133
 RESULT 13
 AAW06107
 ID AAW06107 standard; Protein; 203 AA.
 XX
 AC AAW06107;
 XX
 DT 01-FEB-1997 (first entry)
 XX
 DE Foetal myelin basic protein MBP+X2Cys81/bact.
 XX
 KW Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KW T-lymphocyte; T-cell; anergy; apoptosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 60..85
 FT /label= X2
 FT /note= "exon 2-encoded region"
 XX
 PN WO9634622-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 22-APR-1996; 96WO-US05611.
 XX
 PR 07-JUN-1995; 95US-0482114.
 PR 02-MAY-1995; 95US-0431644.
 PR 02-MAY-1995; 95US-0431648.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 XX
 DR WPI: 1996-505898/50.
 DR N-PSDB; AAT41896.
 XX

PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 XX
 PS Disclosure; Page 81-82; 156pp; English.
 XX
 CC A 21.5 kDa foetal isoform (AAW06107) of myelin basic protein,
 CC MBP+X2Cys81/bact., is the product of a DNA construct (AAT41896)
 CC based on the human foetal MBP+X2Cys81 isoform (AAW00399) but
 CC utilising bacterially-preferred codons in place of the native human
 CC codons (see also AAT41899). This increases prodn. of the MBP in E.
 CC coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also
 CC AAW00399 and AAW06108) are useful in the clinical assessment, diagnosis
 CC and treatment of MS.
 XX Sequence 203 AA;
 SQ
 Query Match 100.0%; Score 260; DB 17; Length 203;
 Best Local Similarity 100.0%; Pred. No. 3.8e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHPARTAHYGSILPOKSHGRTOEDNPVHFFKNIVTPTPPSQGKG 46
 Db 88 hhpatahygsilpqkshgrtqdenpvvhffknivtprtppsqgkg 133
 RESULT 14
 AAW06108
 ID AAW06108 standard; Protein; 203 AA.
 XX
 AC AAW06108;
 XX
 DT 01-FEB-1997 (first entry)
 XX
 DE Foetal myelin basic protein MBP+X2Ser81/bact.
 XX
 KW Myelin basic protein; MBP; MBP+X2Ser81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KW T-lymphocyte; T-cell; anergy; apoptosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 60..85
 FT /label= X2
 FT /note= "exon 2-encoded region, with Cys81Ser
 FT mutation"
 FT Peptide 198..203
 FT /label= Hexa-histidine-tag
 FT /note= "the hexa-histidine tag facilitates
 FT purification of the recombinant protein
 FT from host cells"
 XX
 PN WO9634622-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 22-APR-1996; 96WO-US05611.
 XX
 PR 07-JUN-1995; 95US-0482114.
 PR 02-MAY-1995; 95US-0431644.
 PR 02-MAY-1995; 95US-0431648.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 XX
 DR WPI: 1996-505898/50.
 DR N-PSDB; AAT41897.
 XX

PT New human myelin basic protein and proteolipid protein variant(s) -
PT used in the assessment, diagnosis and treatment of multiple
PT sclerosis
XX
PS Disclosure; Page 82-83; 156pp; English.
XX
CC A 21.5 kDa foetal isoform (AAW06108) of myelin basic protein,
CC MBP-X2Ser81/bact., is the product of a DNA construct (AAT41897)
CC based on the human foetal MBP-X2Cys81 isoform (AAW00399) but
CC utilising codons that are highly expressed in bacterial genes in
CC place of the native codons (see also AAT41889) and incorporating a
CC sequence coding for a hexa-histidine tail. This allows large-
CC scale prodn. and purification of the MBP in bacterial hosts.
CC Recombinant MBP 21.5 polypeptides (see also AAW00399 and AAW06107) are
CC useful in the clinical assessment, diagnosis and treatment of MS.
XX
SQ Sequence 203 AA;

Query Match 100.0%; Score 260; DB 17; Length 203;
Best Local Similarity 100.0%; Pred. No. 3.8e-26;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPKQSHGRQTQDENPWHFFKNIVTPTPPSQKG 46
|||||
Db 88 hhpatahaglsplqskshgrtqdenpvhffknivtprtppsqkg 133
|||||

RESULT 15
AAW06103
ID AAW06103 standard; Protein; 373 AA.
XX
AC AAW06103;
XX
DT 01-FEB-1997 (first entry)
XX
DE MP4 chimera (MBP21.5-delta PLP4 fusion).
XX
KW Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;
KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
KW therapy: T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..368
FT Protein /note= "preferred protein of the invention"
FT Domain 1..197
FT /label= MBP21.5
FT Peptide 198..200
FT /label= Spacer
FT Domain 201..373
FT /label= Delta_PLP4
FT Peptide 201..205
FT /note= "synthetic N-terminal peptide not found in
FT the native protein"
FT Region 208..219
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT Region 210..230
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT Region 241..261
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT Region 242..259
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT Region 244..257
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FT /note= "PLP epitope associated with MS"
FT Region 248..269
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FT Region 248..269
FT /label= Epitope

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256..269
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292..304
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369..373
/label= Histidine_tag
/label= "hexa-histidine tag facilitates recombinant
protein purification"

WO9634622-A1.
07-NOV-1996.
22-APR-1996; 96WO-US05611.
07-JUN-1995; 95US-0482114.
02-MAY-1995; 95US-0431644.
02-MAY-1995; 95US-0431648.
(ALEX-) ALEXION PHARM INC.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
XX
DR WPT; 1996-505898/50.
DR N-PSDB; AAT41893.
XX
PT New human myelin basic protein and proteolipid protein variant(s) -
PT used in the assessment, diagnosis and treatment of multiple
PT sclerosis
XX
PS Claim 34; Page 110-112; 156pp; English.

XX MP4 chimera (AAW06103) is a fusion protein composed of human myelin
 CC basic protein (MBP) foetal isoform MBP21.5 (see also AAW00399) and
 CC delta PLP4 (AAW06101), a proteolipid protein (PLP) mutein that lacks
 CC all 4 hydrophobic domains of native human PLP (AAW06106) but
 CC includes PLP epitopes associated with multiple sclerosis (MS). It
 CC can be expressed in E. coli transformants using a DNA construct
 CC (AAW41893) contg. the MBP21.5-delta PLP4 gene fusion. MP4 chimera
 CC and other novel PLP/MBP21.5 polypeptides (AAW00399-400, AAW06101-08)
 CC are useful for the clinical assessment, diagnosis and treatment
 CC of MS.
 XX
 SQ Sequence 373 AA;

Query Match 100.0%; Score 260; DB 17; Length 373;
 Best Local Similarity 100.0%; Pred. No. 7.6e-26;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQKKG 46
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 88 hhpatahygslpqlkshgrtqdenpvvhffknivtprtpppsqkg 133

Search completed: August 28, 2002, 16:35:03
 Job time: 285 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:32:18 ; Search time 20.54 Seconds
(without alignments)
54.702 Million cell updates/sec

Title: US-09-813-383-1
Perfect score: 260

Sequence: 1 HHPARTAHYGLPQKSHGRT.....VHEFFKNIVTPRPPPSQKG 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCRUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 260 | 100.0 | 170 | 2 | US-08-327-357A-1 |
| 2 | 260 | 100.0 | 170 | 3 | US-09-007-520-1 |
| 3 | 260 | 100.0 | 170 | 4 | US-09-055-263-1 |
| 4 | 260 | 100.0 | 170 | 4 | US-09-007-520-1 |
| 5 | 260 | 100.0 | 170 | 4 | US-08-342-408B-2 |
| 6 | 260 | 100.0 | 171 | 2 | US-08-781-122-2 |
| 7 | 260 | 100.0 | 171 | 4 | US-09-137-759-2 |
| 8 | 234 | 90.0 | 168 | 6 | 5194425-4 |
| 9 | 220.5 | 84.8 | 170 | 1 | US-08-227-372-1 |
| 10 | 220.5 | 84.8 | 170 | 3 | US-08-462-351-3 |
| 11 | 220.5 | 84.8 | 170 | 6 | 5194425-3 |
| 12 | 219.5 | 84.4 | 170 | 3 | US-08-470-397-1 |
| 13 | 198 | 76.2 | 40 | 3 | US-08-297-395-2 |
| 14 | 195.5 | 75.2 | 170 | 6 | 5468481-3 |
| 15 | 135 | 51.9 | 24 | 2 | US-08-480-190-46 |
| 16 | 135 | 51.9 | 24 | 2 | US-08-488-379-46 |
| 17 | 135 | 51.9 | 24 | 5 | PCT-US93-07545-46 |
| 18 | 128 | 49.2 | 23 | 1 | US-08-787-547-1 |
| 19 | 128 | 49.2 | 24 | 1 | US-08-305-871A-2 |
| 20 | 115 | 44.2 | 20 | 3 | US-08-297-395-20 |
| 21 | 112 | 43.1 | 20 | 2 | US-08-640-344-6 |
| 22 | 110 | 42.3 | 20 | 1 | US-08-787-547-35 |
| 23 | 110 | 42.3 | 20 | 3 | US-08-297-395-21 |
| 24 | 108 | 41.5 | 20 | 2 | US-08-640-344-4 |
| 25 | 107 | 41.2 | 19 | 2 | US-08-640-344-2 |
| 26 | 107 | 41.2 | 19 | 2 | US-08-468-540B-9 |
| 27 | 107 | 41.2 | 19 | 3 | US-08-297-395-1 |

28 107 41.2 19 4 US-09-024-220-2 Sequence 2, Appli
29 107 41.2 19 4 US-08-960-190A-32 Sequence 32, Appli
30 107 41.2 19 4 US-08-449-728-2 Sequence 2, Appli
31 107 41.2 20 2 US-08-640-344-1 Sequence 1, Appli
32 107 41.2 20 2 US-08-640-344-3 Sequence 3, Appli
33 107 41.2 20 2 US-08-640-344-5 Sequence 5, Appli
34 107 41.2 20 2 US-08-640-344-7 Sequence 7, Appli
35 107 41.2 20 2 US-08-468-540B-7 Sequence 7, Appli
36 107 41.2 20 4 US-08-960-190A-28 Sequence 28, Appli
37 103.5 39.8 26 1 US-08-227-372-2 Sequence 2, Appli
38 103.5 39.8 26 3 US-08-470-397-2 Sequence 3, Appli
39 102 39.2 20 1 US-08-227-372-3 Sequence 3, Appli
40 102 39.2 20 2 US-08-468-540B-8 Sequence 8, Appli
41 102 39.2 20 3 US-08-470-397-3 Sequence 3, Appli
42 101 38.8 18 2 US-08-468-540B-17 Sequence 17, Appli
43 100 38.5 19 2 US-08-468-540B-18 Sequence 18, Appli
44 100 38.5 19 2 US-08-468-540B-24 Sequence 24, Appli
45 96 36.9 17 2 US-08-468-540B-19 Sequence 19, Appli

ALIGNMENTS

RESULT 1
US-08-327-357A-1
; Sequence 1, Application US/08327357A
; Patent No. 5817629
; GENERAL INFORMATION:
; APPLICANT: WARREN, Kenneth G.
; APPLICANT: CATZ, Ingrid
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
; TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,357A
; FILING DATE: 21-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/798,099
; FILING DATE: 27-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 27052-115469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:

CLONE: human myelin basic protein
US-08-327-357A-1

Query Match 100.0%; Score 260; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.le-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSLPQKSHGRTQDENPVVHFFKNIIVTRTPPPSQGK 46
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DB 61 HHPARTAHYGLSLPQKSHGRTQDENPVVHFFKNIIVTRTPPPSQGK 106
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RESULT 2
US-09-007-520-1
; Sequence 1, Application US/09007520
; Patent No. 6103696
; GENERAL INFORMATION:
; APPLICANT: WARREN, Kenneth G.
; APPLICANT: CATZ, Ingrid
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
; TITLE OF INVENTION: PEPTIDES TO MUTIPLE SCLEROSIS PATIENTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,520
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,357
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 27052-115469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: human myelin basic protein
; US-09-007-520-1

Query Match 100.0%; Score 260; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.le-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSLPQKSHGRTQDENPVVHFFKNIIVTRTPPPSQGK 46
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DB 61 HHPARTAHYGLSLPQKSHGRTQDENPVVHFFKNIIVTRTPPPSQGK 106

RESULT 3
US-09-055-263-1
; Sequence 1, Application US/09055263
; Patent No. 6252040
; GENERAL INFORMATION:
; APPLICANT: WARREN, Kenneth G.
; APPLICANT: CATZ, Ingrid
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
; TITLE OF INVENTION: PEPTIDES TO MUTIPLE SCLEROSIS PATIENTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,263
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,357
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: US 07/798,099
; FILING DATE: 27-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 27052-115469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: human myelin basic protein
; US-09-055-263-1

Query Match 100.0%; Score 260; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.le-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSLPQKSHGRTQDENPVVHFFKNIIVTRTPPPSQGK 46
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DB 61 HHPARTAHYGLSLPQKSHGRTQDENPVVHFFKNIIVTRTPPPSQGK 106
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RESULT 4
US-09-007-520-1
; Sequence 1, Application US/09007520
; Patent No. 6258781
; GENERAL INFORMATION:

APPLICANT: WARREN, Kenneth G.
CATZ, Ingrid
TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/007.520
FILING DATE: 15-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,357
FILING DATE: <Unknown>
APPLICATION NUMBER: CA 2,053,799-0
FILING DATE: 22-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 27052-115469
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: human myelin basic protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-007-520-1

Query Match 100.0%; Score 260; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.le-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIVTPRTPPPSQKG 46
|||||
Db 61 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIVTPRTPPPSQKG 106

RESULT 5
US-08-342-408B-2
Sequence 2, Application US/08342408B
Patent No. 6329499
GENERAL INFORMATION:
APPLICANT: Ling, Nicholas
APPLICANT: Gaur, Amitabh
APPLICANT: Conlon, Paul J.
APPLICANT: Steilman, Lawrence
TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC
PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,408B
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 6329499tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 690068.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-342-408B-2

Query Match 100.0%; Score 260; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.le-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIVTPRTPPPSQKG 46
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Db 61 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIVTPRTPPPSQKG 106

RESULT 6
US-08-781-122-2
Sequence 2, Application US/08781122
Patent No. 5948764
GENERAL INFORMATION:
APPLICANT: Gaur, Amitabh
APPLICANT: Conlon, Paul J.
APPLICANT: Ling, Nicholas
TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS
UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,122
FILING DATE: 09-JAN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 690068.418C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031

;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-122-2

Query Match 100.0%; Score 260; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.1e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTPTPPSQGK 46
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DB 62 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTPTPPSQGK 107
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RESULT 7
US-09-137-759-2
; Sequence 2, Application US/09137759
; Patent No. 6251396
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; FILE REFERENCE: 69068.405C1
; CURRENT APPLICATION NUMBER: US/09/137,759
; CURRENT FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-137-759-2

Query Match 100.0%; Score 260; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.1e-27;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTPTPPSQGK 46
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DB 62 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTPTPPSQGK 107
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RESULT 8
5194425-4
; Patent No. 5194425
; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
; BRIAN R.
; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
; AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/367,751
; FILING DATE: 21-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; SEQ ID NO: 4
; LENGTH: 168
5194425-4

Query Match 90.0%; Score 234; DB 6; Length 168;
Best Local Similarity 93.5%; Pred. No. 6.1e-24;
Matches 43; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTPTPPSQGK 46
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DB 59 HHAARTAHYGLSPQKSHGRQTQDENPVVHFFKNIIVTPTPPSQGK 104
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RESULT 9
US-08-227-372-1
; Sequence 1, Application US/08227372
; Patent No. 5763585
; GENERAL INFORMATION:
; APPLICANT: Nag, Bishwajit
; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
; MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,372
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136,216
; FILING DATE: 13-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14058-32-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; NAME/KEY: Protein
; LOCATION: 1..170
; OTHER INFORMATION: /note= "Myelin basic protein"
US-08-227-372-1

Query Match 84.8%; Score 220.5; DB 1; Length 170;
Best Local Similarity 87.2%; Pred. No. 3.9e-22;
Matches 41; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 HHPARTAHYGLSPQKSHG-RTQDENPVVHFFKNIIVTPTPPSQGK 46
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DB 60 HHAARTHGLSPQKSHGRQDENPVVHFFKNIIVTPTPPSQGK 106
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RESULT 10
US-08-462-351-3
; Sequence 3, Application US/08462351
; Patent No. 6106840
; GENERAL INFORMATION:
; APPLICANT: Sharma, Somesh D.
; APPLICANT: Clark, Brian R.
; APPLICANT: Lerch, Bernard L.
; TITLE OF INVENTION: MHC Conjugates Useful in Ameliorating
; Autoimmunity

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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:33:48 ; Search time 205.27 Seconds
(without alignments)
78.877 Million cell updates/sec

Title: US-09-813-383-1
Perfect score: 260
Sequence: 1 HHPARTAHYGLPQKSHGRT.....VHFKNIVTPRTPPSQK 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main.*
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25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 260 | 100.0 | 46 | 22 | US-09-813-383-1 |
| 2 | 260 | 100.0 | 108 | 21 | US-09-760-443-1465 |
| 3 | 260 | 100.0 | 108 | 21 | US-09-760-495-898 |
| 4 | 260 | 100.0 | 170 | 3 | US-07-798-099A-1 |
| 5 | 260 | 100.0 | 170 | 6 | US-08-241-246-1 |
| 6 | 260 | 100.0 | 170 | 6 | US-08-241-246B-1 |
| 7 | 260 | 100.0 | 170 | 7 | US-08-327-357-1 |

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| 8 | 260 | 100.0 | 170 | 7 | US-08-328-224-5 | Sequence 5, Appli |
| 9 | 260 | 100.0 | 170 | 7 | US-08-342-078-2 | Sequence 2, Appli |
| 10 | 260 | 100.0 | 170 | 8 | US-08-404-228-1 | Sequence 1, Appli |
| 11 | 260 | 100.0 | 170 | 8 | US-08-462-941A-1 | Sequence 1, Appli |
| 12 | 260 | 100.0 | 170 | 8 | US-08-463-412-1 | Sequence 1, Appli |
| 13 | 260 | 100.0 | 170 | 8 | US-08-463-456-1 | Sequence 1, Appli |
| 14 | 260 | 100.0 | 170 | 8 | US-08-481-938-1 | Sequence 1, Appli |
| 15 | 260 | 100.0 | 170 | 24 | US-10-015-540-2 | Sequence 2, Appli |
| 16 | 260 | 100.0 | 171 | 1 | PCT-US00-06233-4 | Sequence 4, Appli |
| 17 | 260 | 100.0 | 171 | 7 | US-08-342-078A-2 | Sequence 2, Appli |
| 18 | 260 | 100.0 | 171 | 8 | US-08-484-409-2 | Sequence 2, Appli |
| 19 | 260 | 100.0 | 171 | 13 | US-08-953-937-2 | Sequence 2, Appli |
| 20 | 260 | 100.0 | 171 | 16 | US-09-218-277-12 | Sequence 12, Appli |
| 21 | 260 | 100.0 | 171 | 16 | US-09-267-590-4 | Sequence 4, Appli |
| 22 | 260 | 100.0 | 171 | 17 | US-09-314-161-12 | Sequence 12, Appli |
| 23 | 260 | 100.0 | 171 | 17 | US-09-378-244-2 | Sequence 2, Appli |
| 24 | 260 | 100.0 | 171 | 22 | US-09-893-348-12 | Sequence 12, Appli |
| 25 | 260 | 100.0 | 171 | 23 | US-09-947-770-4 | Sequence 4, Appli |
| 26 | 260 | 100.0 | 171 | 23 | US-09-989-476-2 | Sequence 2, Appli |
| 27 | 260 | 100.0 | 171 | 24 | US-10-000-439-12 | Sequence 12, Appli |
| 28 | 260 | 100.0 | 176 | 1 | PCT-US01-14827-13007 | Sequence 13007, A |
| 29 | 260 | 100.0 | 183 | 1 | PCT-US01-08656-9330 | Sequence 9330, Ap |
| 30 | 260 | 100.0 | 186 | 17 | US-09-310-707A-28 | Sequence 28, Appli |
| 31 | 260 | 100.0 | 197 | 19 | US-09-512-563-54 | Sequence 54, Appli |
| 32 | 260 | 100.0 | 197 | 19 | US-09-512-563A-54 | Sequence 54, Appli |
| 33 | 260 | 100.0 | 197 | 19 | US-09-512-563C-54 | Sequence 1, Appli |
| 34 | 260 | 100.0 | 203 | 18 | US-09-463-186-1 | Sequence 1502, Ap |
| 35 | 260 | 100.0 | 315 | 21 | US-09-760-443-1502 | Sequence 1779, Ap |
| 36 | 260 | 100.0 | 325 | 21 | PCT-US01-14827-13008 | Sequence 13008, A |
| 37 | 260 | 100.0 | 325 | 21 | PCT-US01-14827-13008 | Sequence 3, Appli |
| 38 | 254 | 97.7 | 167 | 3 | US-07-987-751-3 | Sequence 4, Appli |
| 39 | 254 | 97.7 | 168 | 3 | US-07-987-751-4 | Sequence 1, Appli |
| 40 | 252 | 96.9 | 170 | 3 | US-07-798-099-1 | Sequence 2, Appli |
| 41 | 233.5 | 89.8 | 170 | 5 | US-08-136-216-2 | Sequence 7, Appli |
| 42 | 232 | 89.2 | 168 | 3 | US-07-987-751-7 | Sequence 5, Appli |
| 43 | 226.5 | 87.1 | 169 | 3 | US-07-987-751-5 | Sequence 6, Appli |
| 44 | 226.5 | 87.1 | 172 | 3 | US-07-987-751-6 | Sequence 1, Appli |
| 45 | 220.5 | 84.8 | 170 | 5 | US-08-136-216-1 | |

ALIGNMENTS

RESULT 1
US-09-813-383-1
; Sequence 1, Application US/09813383
; GENERAL INFORMATION:
; APPLICANT: WARREN, KENNETH G.
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND
; THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO
; PATIENTS
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS
; FILE REFERENCE: 09810/027 8741
; CURRENT APPLICATION NUMBER: US/09/813,383
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-813-383-1

Query Match 100.0%; Score 260; DB 22; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.2e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPRTPPSQK 46
|||||
DB 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPRTPPSQK 46
|||||

; FILING DATE: 15-MAY-1992
 ; APPLICATION NUMBER: 07/857,331
 ; FILING DATE: 25-MARCH-1992
 ; APPLICATION NUMBER: 07/662,276
 ; FILING DATE: 28-FEBRUARY-1991
 ; APPLICATION NUMBER: 07/431,565
 ; FILING DATE: 11-MARCH-1989
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: IMI-053 (084.00S)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-5941
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 170 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-241-246-1

Query Match 100.0%; Score 260; DB 6; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIIVTPTPPPSQKG 46
 Db 61 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIIVTPTPPPSQKG 106

RESULT 6
 US-08-241-246B-1
 ; Sequence 1, Application US/08241246B
 ; GENERAL INFORMATION:
 ; APPLICANT: Smilek, Dawn; Hsu, Di-Hwei; and Shi, Jia-Dong
 ; TITLE OF INVENTION: COMPOSITIONS AND TREATMENT FOR
 ; TITLE OF INVENTION: MULTIPLE SCLEROSIS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII-text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/241,246B
 ; FILING DATE: 10-MAY-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/006,116
 ; FILING DATE: 15-JANUARY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: IMI-053 (084.00S)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 742-4214
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 170 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: Internal

US-08-241-246B-1

Query Match 100.0%; Score 260; DB 6; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIIVTPTPPPSQKG 46
 Db 61 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIIVTPTPPPSQKG 106

RESULT 7
 US-08-327-357-1
 ; Sequence 1, Application US/08327357
 ; GENERAL INFORMATION:
 ; APPLICANT: WARREN, Kenneth G.
 ; APPLICANT: CATZ, Ingrid
 ; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN
 ; TITLE OF INVENTION: BASIC PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC
 ; TITLE OF INVENTION: PROTEIN PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue, N.W.
 ; CITY: Washington, D.C.
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3917
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/327,357
 ; FILING DATE: 21-OCT-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: CA 2,053,799-0
 ; FILING DATE: 22-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jeffrey L. Innen
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 18760-95536(temp)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)962-4800
 ; TELEFAX: (202)962-8300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 170 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: homo sapien
 ; IMMEDIATE SOURCE:
 ; CLONE: human myelin basic protein
 ; US-08-327-357-1

Query Match 100.0%; Score 260; DB 7; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIIVTPTPPPSQKG 46
 Db 61 HHPARTAHYGLPQKSHGRQTQDENPVVHFFKNIIVTPTPPPSQKG 106

RESULT 8
 US-08-328-224-5

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; Sequence 5, Application US/08328224
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn
; APPLICANT: Samson, Michael
; APPLICANT: Gefter, Malcolm
; APPLICANT: Hsu, Di-Hwei
; APPLICANT: Shi, Jia-Dong
; APPLICANT: Pallard, Xavier
; APPLICANT: Devaux, Brigitte
; APPLICANT: Rothbard, Jonathan
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING TO HUMANS SUFFERIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,224
; FILING DATE: 10-25-94
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragoras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 094.0 US (IMI-056)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-328-224-5

Query Match 100.0%; Score 260; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQKG 46
Db 61 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQKG 106

RESULT 9
US-08-342-078-2
; Sequence 2, Application US/08342078
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ling, Nicholas
; APPLICANT: Conlon, Paul J.
; APPLICANT: Gaur, Amitabh
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
; TITLE OF INVENTION: SCLEROSIS USING PEPTIDE ANALOGUES AT POSITION 91 OF HUMAN
; TITLE OF INVENTION: MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA

Query Match 100.0%; Score 260; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQKG 46
Db 61 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQKG 106

RESULT 9
US-08-342-078-2
; Sequence 2, Application US/08342078
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ling, Nicholas
; APPLICANT: Conlon, Paul J.
; APPLICANT: Gaur, Amitabh
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
; TITLE OF INVENTION: SCLEROSIS USING PEPTIDE ANALOGUES AT POSITION 91 OF HUMAN
; TITLE OF INVENTION: MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA

Query Match 100.0%; Score 260; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQKG 46
Db 61 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQKG 106

RESULT 10
US-08-404-228-1
; Sequence 1, Application US/08404228
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn
; APPLICANT: Samson, Michael F.;
; APPLICANT: Gefter, Malcolm;
; APPLICANT: Hsu, Di-Hwei;
; APPLICANT: Shi, Jia-Dong;
; APPLICANT: Pallard, Xavier;
; APPLICANT: Devaux, Brigitte;
; APPLICANT: Rothbard, Jonathan; and
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: Compositions and Treatment for Multiple
; TITLE OF INVENTION: Sclerosis
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,228
; FILING DATE: 15-March-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anne I. Craig
; REGISTRATION NUMBER: Reg. No. 32, 976
; REFERENCE/DOCKET NUMBER: 094.1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
```

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; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,078
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nottenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 690068.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELETYPE: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-342-078-2

Query Match 100.0%; Score 260; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQKG 46
Db 61 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPTPTPPSQKG 106

RESULT 10
US-08-404-228-1
; Sequence 1, Application US/08404228
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn
; APPLICANT: Samson, Michael F.;
; APPLICANT: Gefter, Malcolm;
; APPLICANT: Hsu, Di-Hwei;
; APPLICANT: Shi, Jia-Dong;
; APPLICANT: Pallard, Xavier;
; APPLICANT: Devaux, Brigitte;
; APPLICANT: Rothbard, Jonathan; and
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: Compositions and Treatment for Multiple
; TITLE OF INVENTION: Sclerosis
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,228
; FILING DATE: 15-March-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anne I. Craig
; REGISTRATION NUMBER: Reg. No. 32, 976
; REFERENCE/DOCKET NUMBER: 094.1 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
```

TELEFAX: (617) 466-6010
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-404-228-1

Query Match 100.0% Score 260; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFKNIVTPTPTPPSQGK 46
 Db 61 HHPARTAHYGLPQKSHGRGTQDENPVVHFKNIVTPTPTPPSQGK 106

RESULT 11
 US-08-462-941A-1

; Sequence 1, Application US/08462941A
 ; GENERAL INFORMATION:
 ; APPLICANT: Smilek, Dawn;
 ; APPLICANT: Samson, Michael F.;
 ; APPLICANT: Geffer, Malcolm;
 ; APPLICANT: Hsu, Di-Hwei;
 ; APPLICANT: Shi, Jia-Dong;
 ; APPLICANT: Pallard, Xavier;
 ; APPLICANT: Devaux, Brigitte;
 ; APPLICANT: Rothbard, Jonathan; and
 ; APPLICANT: Franzen, Henry M.
 ; TITLE OF INVENTION: Sclerosis
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462.941A
 FILING DATE: 5-June-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/404,228
 FILING DATE: 15-March-1995
 APPLICATION NUMBER: US 08/328,224
 FILING DATE: 25-October-1994
 APPLICATION NUMBER: US 08/300,811
 FILING DATE: 1-September-1994
 APPLICATION NUMBER: US 08/241,246
 FILING DATE: 10-May-1994
 APPLICATION NUMBER: US 08/116,824
 FILING DATE: 3-September-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: Reg. No. 36,207
 REFERENCE/DOCKET NUMBER: 094.1 US1 (IMI-052CPDV)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-462-941A-1

Query Match 100.0% Score 260; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.6e-24;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFKNIVTPTPTPPSQGK 46
 Db 61 HHPARTAHYGLPQKSHGRGTQDENPVVHFKNIVTPTPTPPSQGK 106

RESULT 12
 US-08-463-412-1

; Sequence 1, Application US/08463412
 ; GENERAL INFORMATION:
 ; APPLICANT: Smilek, Dawn;
 ; APPLICANT: Samson, Michael F.;
 ; APPLICANT: Geffer, Malcolm;
 ; APPLICANT: Hsu, Di-Hwei;
 ; APPLICANT: Shi, Jia-Dong;
 ; APPLICANT: Pallard, Xavier;
 ; APPLICANT: Devaux, Brigitte;
 ; APPLICANT: Rothbard, Jonathan; and
 ; APPLICANT: Franzen, Henry M.
 ; TITLE OF INVENTION: Compositions and Treatment for Multiple Sclerosis
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463.412
 FILING DATE: 5-June-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/404,228
 FILING DATE: 15-March-1995
 APPLICATION NUMBER: US 08/328,224
 FILING DATE: 25-October-1994
 APPLICATION NUMBER: US 08/300,811
 FILING DATE: 1-September-1994
 APPLICATION NUMBER: US 08/241,246
 FILING DATE: 10-May-1994
 APPLICATION NUMBER: US 08/116,824
 FILING DATE: 3-September-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Amy E. Mandragouras
 REGISTRATION NUMBER: Reg. No. 36,207
 REFERENCE/DOCKET NUMBER: 094.1 USD2 (IMI-052DV2)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 170 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal
 US-08-463-412-1

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Query Match      100.0%; Score 260; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps

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Oy 1 HHPARTAHVGSLLPQKSHGRTQDENPVVHFFKNIVTPRTPPSQSGK 46
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Db 61 HHPARTAHVGSLLPQKSHGRTQDENPVVHFFKNIVTPRTPPSQSGK 106

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RESULT 13
US-08-463-456-1
; Sequence 1, Application US/08463456
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn;
; APPLICANT: Samson, Michael F.;
; APPLICANT: Gefter, Malcolm;;
; APPLICANT: Hsu, Di-Hwei;
; APPLICANT: Shi, Jia-Dong;
; APPLICANT: Pallard, Xavier;
; APPLICANT: Devaux, Brigitte;
; APPLICANT: Rothbard, Jonathan; and
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: Compositions and Treatment for Multiple Sclerosis
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
;

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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,456
FILING DATE: 5-June-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,228
FILING DATE: 15-March-1995
APPLICATION NUMBER: US 08/328,224
FILING DATE: 25-October-1994
APPLICATION NUMBER: US 08/300,811
FILING DATE: 1-September-1994
APPLICATION NUMBER: US 08/241,245
FILING DATE: 10-May-1994
APPLICATION NUMBER: US 08/116,824
FILING DATE: 3-September-1993
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: Reg. No. 36,207
REFERENCE/DOCKET NUMBER: 094.1 US03 (IMI-052DV3)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-463-456-1

| | | | | |
|-----------------------|-----------------|--------------------|--------|-------------|
| Query Match | 100.0% | Score 260; | DB 8; | Length 170; |
| Best Local Similarity | 100.0%; | Pred. No. 1.6e-24; | | |
| Matches 46; | Conservative 0; | Mismatches 0; | Indels | |

QY 1 HHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQKG 46

D**b** 61 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQKG 106

RESULT 14

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US-08-481-938--1
; Sequence 1, Application US/08481938
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn;
; APPLICANT: Samson, Michael F.;
; APPLICANT: Gelter, Malcolm;
; APPLICANT: Hsu, Di-Hwei;
; APPLICANT: Shi, Jia-Dong;
; APPLICANT: Pallard, Xavier;
; APPLICANT: Devaux, Brigitte;
; APPLICANT: Rothbard, Jonathan; and
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: Compositions and Treatment for Multiple Sclerosis
; NUMBER OF SEQUENCES: 71

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,938
FILING DATE: 7-June-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,228
FILING DATE: 15-March-1995
APPLICATION NUMBER: US 08/328,224
FILING DATE: 25-October-1994
APPLICATION NUMBER: US 08/300,811
FILING DATE: 1-September-1994
APPLICATION NUMBER: US 08/241,246
FILING DATE: 10-May-1994
APPLICATION NUMBER: US 08/116,824
FILING DATE: 3-September-1993
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: Reg. No. 36,200
REFERENCE/DOCKET NUMBER: 094.1 USD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-481-938-1

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Query Match      100.0%; Score 260; DB 8; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HHPARTAHYGSIPQKSHGRQTQDENPVVHFFKNITVPTPTPPSQSGK 46
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Dd 61 HHPARTAHYGSIPQKSHGRQTQDENPVVHFFKNITVPTPTPPSQSGK 106

RESULT 15

US-10-015-540-2
; Sequence 2, Application US/10015540


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; GENERAL INFORMATION:
; APPLICANT: Ling, Nicholas
; Gaur, Amitabh
; Conlon, Paul J.
; Steinman, Lawrence
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
; SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC
; PROTEIN
;
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/015,540
; FILING DATE: 11-Dec-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christensen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 690068.405C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-015-540-2

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Query Match      100.0%; Score 260; DB 24; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRQDENPVWHFFKNIVTPRTPPSQGK 46
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Db 61 HHPARTAHYGLPQKSHGRQDENPVWHFFKNIVTPRTPPSQGK 106

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Search completed: August 28, 2002, 16:39:34
Job time: 346 sec

US-10-143-775-898

Query Match 100.0%; Score 260; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46
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DB 11 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 56

RESULT 3

US-10-212-054-1465
; Sequence 1465, Application US/10212054
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P212CIN
; CURRENT APPLICATION NUMBER: US/10/212,054
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2164
; Prior application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1465
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-054-1465

Query Match 100.0%; Score 260; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.2e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46
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DB 11 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 56

RESULT 4

PCT-US02-13527-12
; Sequence 12, Application PC/TUS0213527
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoheng
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; FILE REFERENCE: UC067.004QPC
; CURRENT APPLICATION NUMBER: PCT/US02/13527
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 10/000,439
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-13527-12

Query Match 100.0%; Score 260; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 5.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46
|||||
DB 62 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 107

RESULT 5

US-10-104-973-2
; Sequence 2, Application US/10104973
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophili
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; FILE REFERENCE: 690068.405C4
; CURRENT APPLICATION NUMBER: US/10/104,973
; CURRENT FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-973-2

Query Match 100.0%; Score 260; DB 6; Length 171;
Best Local Similarity 100.0%; Pred. No. 5.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46
|||||
DB 62 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 107

RESULT 6

US-08-431-644B-4
; Sequence 4, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-4

Query Match 100.0%; Score 260; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 5.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 46
|||||
DB 63 HHPARTAHYGLPQKSHGRTQDENPVVHFFKNIIVTPTPPPSQKG 108

RESULT 7

US-08-431-644C-4
; Sequence 4, Application US/08431644C
; GENERAL INFORMATION:

```

; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-4

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Query Match          100.0%; Score 260; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 5.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
    |||||
Db 63 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 108
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```

```

RESULT 8
US-08-431-644B-1
; Sequence 1, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-1

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Query Match          100.0%; Score 260; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
    |||||
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133
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```

```

RESULT 9
US-08-431-644C-1
; Sequence 1, Application US/08431644C
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.

```

```

; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-1

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Query Match          100.0%; Score 260; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.6e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
    |||||
Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133
    |||||

```

```

RESULT 10
US-08-431-644B-2
; Sequence 2, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-2

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Query Match          100.0%; Score 260; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
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Db 88 HHPARTAHYGLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 133
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```

```

RESULT 11
US-08-431-644B-3
; Sequence 3, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.

```

; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-3

Query Match 100.0%; Score 260; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIIVTPTPTPPSQGK 46
|||||
Db 88 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIIVTPTPTPPSQGK 133
|||||

RESULT 12
US-08-431-644B-27
; Sequence 27, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-27

Query Match 100.0%; Score 260; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIIVTPTPTPPSQGK 46
|||||
Db 88 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIIVTPTPTPPSQGK 133
|||||

RESULT 13
US-08-431-644C-2
; Sequence 2, Application US/08431644C
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.

; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-2

Query Match 100.0%; Score 260; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIIVTPTPTPPSQGK 46
|||||
Db 88 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIIVTPTPTPPSQGK 133
|||||

RESULT 14
US-08-431-644C-3
; Sequence 3, Application US/08431644C
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-3

Query Match 100.0%; Score 260; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIIVTPTPTPPSQGK 46
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Db 88 HHPARTAHYGLSPQKSHGRTQDENPVVHFFKNIIVTPTPTPPSQGK 133
|||||

RESULT 15
US-08-431-644C-27
; Sequence 27, Application US/08431644C
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644C

. Thu Aug 29 10:03:54 2002

; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-27

Query Match 100.0%; Score 260; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.8e-24;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHPARTAHYGSILPOKSHGRTQDENPVVHFFKNIYVTRTPPPSGKG 46
Db 88 HHPARTAHYGSILPOKSHGRTQDENPVVHFFKNIYVTRTPPPSGKG 133

Search completed: August 28, 2002, 16:40:33
Job time: 385 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 16:33:08 ; Search time 25.27 seconds
(without alignments)
174.915 Million cell updates/sec

Title: US-09-813-383-1
Perfect score: 260
Sequence: 1 HHPARTAHYSLPKSHGRT.....VHFKNIVTPRTPPSQKG 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 260 | 100.0 | 197 | 1 MBHUB | myelin basic prote |
| 2 | 242 | 93.1 | 171 | 1 MBPGB | myelin basic prote |
| 3 | 228.5 | 87.9 | 171 | 1 MBPGB | myelin basic prote |
| 4 | 220.5 | 84.8 | 169 | 1 MBPGB | myelin basic prote |
| 5 | 219.5 | 84.4 | 167 | 2 A37246 | myelin basic prote |
| 6 | 218.5 | 84.0 | 328 | 1 MBMSB | goli-myelin basic |
| 7 | 204.5 | 78.7 | 128 | 1 MBRTS | myelin basic prote |
| 8 | 181.5 | 69.8 | 174 | 2 S08535 | myelin basic prote |
| 9 | 116 | 44.6 | 42 | 2 B92087 | myelin basic prote |
| 10 | 80.5 | 31.0 | 155 | 2 B32999 | myelin basic prote |
| 11 | 78.5 | 30.2 | 128 | 2 A60215 | myelin basic prote |
| 12 | 77 | 29.6 | 14 | 2 S12904 | protein kinase (PC |
| 13 | 65.5 | 25.2 | 154 | 2 S55017 | hypothetical prote |
| 14 | 63 | 24.2 | 632 | 2 F83387 | copper resistance |
| 15 | 62 | 23.8 | 295 | 2 S58850 | homeotic protein a |
| 16 | 60 | 23.1 | 667 | 1 VCLJGL | env polyprotein pr |
| 17 | 59 | 22.7 | 556 | 2 A81931 | probable adhesin N |
| 18 | 59 | 22.7 | 736 | 2 E71414 | hypothetical prote |
| 19 | 58.5 | 22.5 | 445 | 2 A56024 | GDP dissociation i |
| 20 | 56.5 | 21.7 | 159 | 2 AC2254 | hypothetical prote |
| 21 | 56.5 | 21.7 | 444 | 2 A55071 | hydrogen peroxide- |
| 22 | 56 | 21.5 | 562 | 2 T28858 | hypothetical prote |
| 23 | 55.5 | 21.3 | 218 | 2 F86939 | probable lipoprote |
| 24 | 55.5 | 21.3 | 263 | 2 A23659 | spectrin beta chai |
| 25 | 55.5 | 21.3 | 680 | 1 XJBVTK | transketolase (EC |
| 26 | 55 | 21.2 | 257 | 2 D82350 | ribonuclease PH VC |
| 27 | 55 | 21.2 | 422 | 2 T09742 | drought-induced pr |
| 28 | 55 | 21.2 | 891 | 2 G82543 | conserved hypothet |
| 29 | 55 | 21.2 | 2061 | 2 T13751 | transcription fact |

ALIGNMENTS

RESULT 1

MBHUB
myelin basic protein [validated] - human
N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein p
.5K splice form
C:Species: Homo sapiens (man)
C:Date: 18-Dec-1981 #sequence_revision 25-Aug-1995 #text_change 20-Apr-2001
C:Accession: S10482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219;
R:Streich, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 370, 503-510, 1989
A:Title: The organization of the human myelin basic protein gene. Comparison with the
A:Reference number: S10482; MUID:89302693
A:Accession: S10482
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-197 <SPR>
A:Cross-references: EMBL:X17286; NID:g34490; PIDN:CAA35179.1; PID:g1184244
R:Kamholz, J.; de Ferr, F.; Puckett, C.; Lazzarini, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986
A:Title: Identification of three forms of human myelin basic protein by cDNA cloning.
A:Reference number: A94106; MUID:86259714
A:Accession: A94106
A:Molecule type: mRNA
A:Residues: 1-59,86-197 <KAM>
A:Cross-references: GB:M13577; NID:g187408; PIDN:AAA59562.1; PID:g307160
A:Note: 18.5K splice form
A:Accession: B94106
A:Molecule type: mRNA
A:Residues: 1-197 <KA2>
A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form
A:Note: a 17.2K splice form is also described
A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K
Biochem. J. 123, 57-67, 1971
A:Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.
A:Reference number: A90256; MUID:72066400
A:Accession: A90256
A:Molecule type: protein
A:Residues: 2-59,86-197 <CAR>
R:Proost, P.; Van Damme, J.; Opdenakker, G.
Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993
A:Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin b
A:Reference number: JH0802; MUID:93282820
A:Accession: JH0802
A:Molecule type: protein
A:Residues: 2-59,86-197 <PRO>
R:Scoble, H.A.; Whitaker, J.N.; Blemann, K.
J. Neurochem. 47, 614-616, 1986
A:Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44
A:Reference number: A60862; MUID:86280476
A:Accession: A60862

nerve growth facto
hypothetical prote
histidinol-phospha
hypothetical prote
tRNA nucleotidyltr
protein F6N18.2 [1
probable serine/th
GDP dissociation 1
rab GDP dissociati
hypothetical prote
lipoprotein vsai [1
nerve growth facto
hypothetical prote
hypothetical prote
hypothetical prote
beta-tectorin prec

30 54.5 21.0 243 2 A26311
31 54.5 21.0 282 2 T45618
32 54.5 21.0 336 2 E84311
33 54 20.8 201 2 T35572
34 54 20.8 238 1 A64059
35 54 20.8 291 2 F86451
36 54 20.8 640 1 S37869
37 53.5 20.6 445 2 C56936
38 53.5 20.6 445 2 B54091
39 53.5 20.6 611 2 C84863
40 53.5 20.6 839 2 H90577
41 53 20.4 235 2 S14481
42 53 20.4 316 2 D83233
43 53 20.4 322 2 S28091
44 53 20.4 323 2 T15311
45 53 20.4 329 2 A57246

A:Molecule type: protein
A:Residues: 2-45;117-197 <SCO>
A:Note: evidence for acetylated amino end
R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.
J. Biol. Chem. 259, 5028-5031, 1984
A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by mass spectrometry
A:Reference number: A61420; MUID:84185608
A:Accession: A61420
A:Molecule type: protein
A:Residues: 46-59,86-116 <GIB>
R:Wood, D.D.; Moscarello, M.A.
J. Biol. Chem. 264, 5121-5127, 1989
A:Title: The isolation, characterization, and lipid-aggregating properties of a citrullin
A:Reference number: A33273; MUID:89174797
A:Accession: A33273
A:Molecule type: protein
A:Residues: 15-25, 'X', 27-31, 'X', 33-59,86-148, 'X', 150-156, 'X', 158-185, 'X', 187-196, 'X' <WC>
A:Note: form C-8; residues designated 'X' were determined as citrulline
R:Baldwin, G.S.; Carnegie, P.R.
Biochem. J. 123, 69-74, 1971
A:Title: Isolation and partial characterization of methylated arginines from the encephalomyelinase
A:Reference number: A90257; MUID:72066401
A:Contents: annotation; methylarginine
A:Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approx
R:Lennon, V.A.; Wilks, A.V.; Carnegie, P.R.
J. Immunol. 105, 1223-1230, 1970
A:Reference number: A92806; MUID:71088405
A:Contents: annotation
A:Note: a region including residues 139-149 induces experimental autoimmune encephalomyelitis in the rat
R:Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prusiner, S.B.
Genomics 6, 16-22, 1990
A:Title: Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a new form of
A:Reference number: I54219; MUID:90152679
A:Accession: I54219
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-59 <RES>
A:Cross-references: GB:M63599; NID:g187402; PIDN:AAA59560.1; PID:g187403
R:Roth, H.J.; Kronquist, K.E.; Keriato de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 17, 321-328, 1987
A:Title: Evidence for the expression of four myelin basic protein variants in the developing rat brain
A:Reference number: I56567; MUID:87311781
A:Accession: I56567
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-132,144-197 <RE2>
A:Cross-references: GB:M30516; NID:g187410; PIDN:AAA59563.1; PID:g307161
A:Accession: I73634
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-197 <RE3>
A:Cross-references: GB:M30515; NID:g187412; PIDN:AAA59564.1; PID:g307162
R:Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 16, 227-238, 1986
A:Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin
A:Reference number: I56565; MUID:86308101
A:Accession: I56565
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-59,86-133,145-197 <RE4>
A:Cross-references: GB:M30047; NID:g187400; PIDN:AAA59559.1; PID:g307159
R:Boullas, C.; Pang, H.; Mastroianni, F.; Moscarello, M.A.
Arch. Biochem. Biophys. 322, 174-182, 1995
A:Title: The isolation and characterization of four myelin basic proteins from the unbound myelin fraction of rat brain
A:Reference number: S66383; MUID:96004793
A:Accession: S66383
A:Molecule type: protein
A:Residues: 23-25, 'X', 27-39 <BOU>
C:Comment: Four alternatively spliced forms of myelin basic protein have been observed, C1, C2, C3, and C4
C:Genetics:
A:Gene: GDB:MBP
A:Cross-references: GDB:119379; OMIM:159430
A:Map position: 18q22-18qter

A:Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
C:Function:
A:Description: probably helps maintain myelin structure
C:Superfamily: myelin basic protein
C:Keywords: acetylated amino end; alternative splicing; citrulline; experimental auto
F:2-197/Product: myelin basic protein, 21.5K splice form #status predicted <MAT1>
F:2-132,144-197/Product: myelin basic protein, 20.2K splice form #status predicted <MAT2>
F:2-59,86-197/Product: myelin basic protein, 18.5K splice form #status predicted <MAT3>
F:2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status predicted <MAT4>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experim
F:134/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 260; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 9,2e-25;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSGHRTQDENPVVHFFKNIVTPTPTPPSQGK 46
Db 88 HHPARTAHYGLPQKSGHRTQDENPVVHFFKNIVTPTPTPPSQGK 133

RESULT 2
MBCZB
N:Alin basic protein - chimpanzee (tentative sequence)
N:Alternate names: MBP
C:Species: Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 06-Sep-1996
C:Accession: A03139
R:Westall, F.C.; Thompson, M.; Kalter, S.S.
Life Sci. 17, 219-223, 1975
A:Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.
A:Reference number: A03139; MUID:76009821
A:Accession: A03139
A:Molecule type: protein
A:Residues: 1-171 <MBS>
C:Comment: This protein may function in maintaining the proper structure of myelin.
C:Superfamily: myelin basic protein
C:Keywords: blocked amino end; methylated amino acid; myelin; structural protein
F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
F:107/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg)

Query Match 93.1%; Score 242; DB 1; Length 171;
Best Local Similarity 95.7%; Pred. No. 1.3e-22;
Matches 44; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSGHRTQDENPVVHFFKNIVTPTPTPPSQGK 46
Db 61 HHPARTAHYGLPQKSGHRTQDENPVVHFFKNIVTPTPTPPSQGK 106

RESULT 3
MBPGB
N:Alin basic protein - pig (tentative sequence)
N:Alternate names: myelin Al protein
N:Contains: myelin basic protein amide 14
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Apr-1996 #sequence_revision 26-Apr-1996 #text_change 07-May-1999
C:Accession: A61640; A36245
R:Kira, J.; Delbier, G.E.; Kruttsch, H.C.; Martenson, R.E.
J. Neurochem. 44, 134-142, 1985
A:Title: Amino acid sequence of porcine myelin basic protein.
A:Reference number: A61640; MUID:85056964
A:Accession: A61640
A:Molecule type: protein
A:Residues: 1-171 <KIR>
A:Note: some peptides were ordered by homology
R:Takamatsu, K.; Tatemoto, K.
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.
A:Reference number: A36245; MUID:91058553

[illegible]

0.

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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:35:33 ; Search time 16.25 Seconds
(without alignments)
109.606 Million cell updates/sec

Title: US-09-813-383-1
Perfect score: 260
Sequence: 1 HHPARTAHYGLPQKSHGRT.....VHFFKNIVTPRTPPPSQSGK 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------|--------------------|
| 1 | 260 | 100.0 | 304 | 1 MBP_HUMAN | P02686 homo sapien |
| 2 | 242 | 93.1 | 171 | 1 MBP_PANTR | P06906 pan troglod |
| 3 | 228.5 | 87.9 | 171 | 1 MBP_PIG | P81558 sus scrofa |
| 4 | 220.5 | 84.8 | 169 | 1 MBP_BOVIN | P02687 bos taurus |
| 5 | 219.5 | 84.4 | 167 | 1 MBP_CAVPO | P25188 cavia porce |
| 6 | 218.5 | 84.0 | 250 | 1 MBP_MOUSE | P04370 mus musculu |
| 7 | 216 | 83.1 | 168 | 1 MBP_RABIT | P25274 oryctolagus |
| 8 | 204.5 | 78.7 | 124 | 1 MBP_RAT | P02688 rattus norv |
| 9 | 181.5 | 69.8 | 173 | 1 MBP_CHICK | P15720 gallus gall |
| 10 | 153 | 58.8 | 175 | 1 MBP_XENLA | P87346 xenopus lae |
| 11 | 81 | 31.2 | 154 | 1 MBP_RAJER | Q91325 raja erinac |
| 12 | 81 | 31.2 | 154 | 1 MBP_SQUAC | Q91439 squalus aca |
| 13 | 80.5 | 31.0 | 154 | 1 MBP_HETFR | P20939 heterodontu |
| 14 | 65.5 | 25.2 | 487 | 1 OAF_DROME | Q9n1a6 drosophila |
| 15 | 60 | 23.1 | 667 | 1 ENV_GALV | P21415 gibbon ape |
| 16 | 59.5 | 22.9 | 445 | 1 GDIB_HUMAN | P50395 homo sapien |
| 17 | 58.5 | 22.5 | 405 | 1 HMV_STRUP | O26656 strongyloce |
| 18 | 58.5 | 22.5 | 445 | 1 GDIB_CANPA | O97556 canis famil |
| 19 | 58.5 | 22.5 | 445 | 1 GDIB_MOUSE | P03397 mus musculu |
| 20 | 57.5 | 22.1 | 304 | 1 HEYL_CANPA | Q9ts22 canis famil |
| 21 | 55.5 | 21.3 | 218 | 1 LPQT_MYCLE | Q9cd47 mycobacteri |
| 22 | 55.5 | 21.3 | 679 | 1 TKTL1_YEAST | P23254 saccharomyc |
| 23 | 55 | 21.2 | 555 | 1 DP87_DICDI | Q04503 dictyosteli |
| 24 | 54.5 | 21.0 | 243 | 1 NGF_CHICK | P05200 gallus gall |
| 25 | 54 | 20.8 | 238 | 1 RNPH_HAETN | P44444 haemophilus |
| 26 | 54 | 20.8 | 640 | 1 ELM1_YEAST | P32801 saccharomyc |
| 27 | 53.5 | 20.6 | 445 | 1 GDIC_MOUSE | Q61598 mus musculu |
| 28 | 53.5 | 20.6 | 445 | 1 GDIC_RAT | P50399 rattus norv |
| 29 | 53 | 20.4 | 231 | 1 NGF_XENLA | P21617 xenopus lae |
| 30 | 53 | 20.4 | 247 | 1 Y281_HUMAN | Q92556 homo sapien |
| 31 | 53 | 20.4 | 322 | 1 REPL_ZYGBI | P13777 zygosacchar |
| 32 | 53 | 20.4 | 329 | 1 TECB_CHICK | P54097 gallus gall |
| 33 | 52.5 | 20.2 | 202 | 1 VIC2_AGRTE | P06666 agrobacteri |

RESULT 1

| ID | MBP_HUMAN | STANDARD; | PRT; | 304 AA. |
|----|--|-----------|------|---------|
| AC | P02686; Q15337; Q15338; Q15339; Q15340; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 01-MAR-2002 (Rel. 41, Last annotation update) | | | |
| DE | Myelin basic protein (MBP) (Myelin A1 protein) (Myelin membrane | | | |
| DE | encephalitogenic protein). | | | |
| GN | MBP. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). | | | |
| RC | TISSUE=Brain; | | | |
| RX | MEDLINE=94068468; PubMed=7504278; | | | |
| RA | Pribyl T.M., Campagnoni C.W., Kampf K., Kashima T., Handley V.W., | | | |
| RA | McMahon J., Campagnoni A.T.; | | | |
| RT | "The human myelin basic protein gene is included within a 179-kilobase | | | |
| RT | transcription unit; expression in the immune and central nervous | | | |
| RT | systems." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 90:10695-10699(1993). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 3; 4; 5 AND 6). | | | |
| RC | TISSUE=Embryonic spinal cord; | | | |
| RX | MEDLINE=87311781; PubMed=2442403; | | | |
| RA | Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F., | | | |
| RA | Campagnoni A.T.; | | | |
| RT | "Evidence for the expression of four myelin basic protein variants in | | | |
| RT | the developing human spinal cord through cDNA cloning." | | | |
| RL | J. Neurosci. Res. 17:321-328(1987). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 6). | | | |
| RC | TISSUE=Embryonic spinal cord; | | | |
| RX | MEDLINE=86308101; PubMed=2427738; | | | |
| RA | Roth H.J., Kronquist K.E., Pretorius P.J., Crandall B.F., | | | |
| RA | Campagnoni A.T.; | | | |
| RT | "Isolation and characterization of a cDNA coding for a novel human | | | |
| RT | 17.3K myelin basic protein (MBP) variant." | | | |
| RL | J. Neurosci. Res. 16:227-238(1986). | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 3 AND 5). | | | |
| RC | MEDLINE=86259714; PubMed=2425357; | | | |
| RX | Kamholz J., de Ferra F., Puckett C., Lazzarini R.A.; | | | |
| RA | "Identification of three forms of human myelin basic protein by cDNA | | | |
| RT | cloning." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986). | | | |
| RN | [5] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 3; 4; 5 AND 6). | | | |
| RX | MEDLINE=89302693; PubMed=2472816; | | | |
| RA | Streicher R., Stoffel W.; | | | |
| RT | "The organization of the human myelin basic protein gene. Comparison | | | |
| RT | with the mouse gene." | | | |
| RL | Biol. Chem. Hoppe-Seyler 370:503-510(1989). | | | |

ALIGNMENTS

| | | | | | |
|----|------|------|------|--------------|--------------------|
| 34 | 52.5 | 20.2 | 2128 | 1 SPCB_MOUSE | P15508 mus musculu |
| 35 | 52.5 | 20.2 | 2137 | 1 SPCB_HUMAN | P11277 homo sapien |
| 36 | 52 | 20.0 | 376 | 1 FXL2_HUMAN | P58012 homo sapien |
| 37 | 52 | 20.0 | 479 | 1 YP66_YEAST | Q12194 saccharomyc |
| 38 | 52 | 20.0 | 677 | 1 SGL_HUMAN | P05060 homo sapien |
| 39 | 52 | 20.0 | 1053 | 1 FAKL_CHICK | Q00944 gallus gall |
| 40 | 52 | 20.0 | 2300 | 1 CYAA_NEUCR | Q01631 neurospora |
| 41 | 51.5 | 19.8 | 273 | 1 DLX3_NOTYI | P53770 notophthalm |
| 42 | 51.5 | 19.8 | 1108 | 1 DBS_HUMAN | O15068 homo sapien |
| 43 | 51.5 | 19.8 | 1149 | 1 DBS_MOUSE | Q64096 mus musculu |
| 44 | 51.5 | 19.8 | 1736 | 1 ZOI_HUMAN | Q07157 homo sapien |
| 45 | 51 | 19.6 | 523 | 1 TP6B_METTH | O27088 methanobact |

RX MEDLINE=95377296; PubMed=7544282;
 RA Mendz G.L., Barden J.A., Martenson R.E.;
 RC "Conformation of a tetradecapeptide epitope of myelin basic protein.";
 RA Strausberg R.;
 RL Eur. J. Biochem. 231:659-666(1995).
 RN [17]
 RP 3D-STRUCTURE MODELING OF 135-279 (ISOFORM 5).
 RX MEDLINE=97172499; PubMed=9020143;
 RA Ridsdale R.A., Beniac D.R., Tompkins T.A., Moscarello M.A., Harauz G.;
 RC "Three-dimensional structure of myelin basic protein. II. Molecular
 RA modeling and considerations of predicted structures in multiple
 RT sclerosis.";
 RL J. Biol. Chem. 272:4269-4275(1997).
 RN [18]
 RP FUNCTION: The classic group of MBP isoforms (isoforms 4-14) are
 CC with PIP the most abundant protein components of the myelin
 CC membrane in the CNS. They have a role in both its formation and
 CC stabilization. The smaller isoforms might have an important role
 CC in remyelination of denuded axons in multiple sclerosis. The non-
 CC classic group of MBP isoforms (isoforms 1-3/Golli-MBP) may
 CC preferentially have a role in the early developing brain long
 CC before myelination, maybe as components of transcriptional
 CC complexes, and may also be involved in signaling pathways in T-
 CC cells and neural cells. Differential splicing events combined to
 CC optional posttranslational modifications give a wide spectrum of
 CC isomers, each of them having maybe a specialized function.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -!- ALTERNATIVE PRODUCTS: At least 6 isoforms: 1/Golli-MBP1/HOG7
 CC (shown here), 2/Golli-MBP2/HOG5, 3/MBP1/21.5 kDa, 4/MBP2/20.2 kDa,
 CC 5/MBP3/18.5 kDa and 6/MBP4/17.2 kDa; are produced by alternative
 CC splicing.
 CC -!- TISSUE SPECIFICITY: MBP isoforms are found in both the central and
 CC the peripheral nervous system, whereas Golli-MBP isoforms are
 CC expressed in fetal thymus, spleen and spinal cord, as well as in
 CC cell lines derived from the immune system.
 CC -!- DEVELOPMENTAL STAGE: Expression turns on abruptly in fetus of 14
 CC to 16 weeks. Even smaller isoforms seem to be produced during
 CC embryogenesis. Some of these persisting in the adult. Expression
 CC of MBP2 is more evident at 16 weeks and its relative
 CC proportion declined thereafter.
 CC -!- PTM: Several charge isomers of MBP: C1 (the most cationic, least
 CC modified, and most abundant form), C2, C3, C4, C5, C6, C7, C8-A
 CC and C8-B (the less cationic form); are produced as a result of
 CC optional PTM, such as phosphorylation, deamidation of glutamine or
 CC asparagine, arginine citrullination and methylation. C8-A and C8-B
 CC contain each two mass isoforms termed C8-A(H), C8-A(L), C8-B(H)
 CC and C8-B(L), (H) standing for higher and (L) for lower molecular
 CC weight. C3, C4 and C5 are phosphorylated. The ratio of methylated
 CC arginine residues decreases in aging, making the protein more
 CC cationic.
 CC -!- DISEASE: The reduction in the surface charge of citrullinated
 CC and/or methylated MBP could result in a weakened attachment to the
 CC myelin membrane. This mechanism could be operative in
 CC demyelinating diseases such as chronic multiple sclerosis (MS),
 CC and fulminating MS (Marburg's disease).
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC
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 CC -----
 CC EMBL; L18866; AAA72011.1; -
 CC EMBL; L18865; AAA72010.1; -
 CC EMBL; L18864; AAA72009.1; -
 CC EMBL; L18862; AAA72008.1; -
 CC EMBL; M30516; AAA59563.1; -
 CC EMBL; M30515; AAA59564.1; -
 CC EMBL; M30047; AAA59559.1; -
 CC EMBL; M33577; AAA59562.1; -
 CC EMBL; M20009; AAA59561.1; -
 CC
 DR EMBL; L18866; AAA72011.1; -
 DR EMBL; L18865; AAA72010.1; -
 DR EMBL; L18864; AAA72009.1; -
 DR EMBL; L18862; AAA72008.1; -
 DR EMBL; M30516; AAA59563.1; -
 DR EMBL; M30515; AAA59564.1; -
 DR EMBL; M30047; AAA59559.1; -
 DR EMBL; M33577; AAA59562.1; -
 DR EMBL; M20009; AAA59561.1; -
 DR

RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 5).
 RC TISSUE=Melanoma;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE (ISOFORM 5).
 RX MEDLINE=72066400; PubMed=4108501;
 RA Carnegie P.R.;
 RC "Amino acid sequence of the encephalitogenic basic protein from human
 RA myelin.";
 RL Biochem. J. 123:57-67(1971).
 RN [8]
 RP SEQUENCE OF 135-192 FROM N.A.
 RX MEDLINE=90152679; PubMed=1689270;
 RA Boylan K.B., Ayres T.M., Popko B., Takahashi N., Hood L.E.,
 RA Prusiner S.B.;
 RC "Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a
 RA new form of oligonucleotide repetitive sequence showing length
 RT polymorphism.";
 RL Genomics 6:16-22(1990).
 RN [9]
 RP SEQUENCE OF 179-222 (ISOFORM 5), AND REVISIONS.
 RA Shapira R., McKeally S.S., Chou F., Kibler R.F.;
 RC "Encephalitogenic fragment of myelin basic protein. Amino acid
 RA sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640(1971).
 RN [10]
 RP SEQUENCE OF 135-178 AND 224-304 (ISOFORM 3), AND MASS SPECTROMETRY.
 RX MEDLINE=86280476; PubMed=2426402;
 RA Scoble H.A., Whitaker J.N., Biemann K.;
 RC "Analysis of the primary sequence of human myelin basic protein
 RA peptides 1-44 and 90-170 by fast atom bombardment mass spectrometry.";
 RL J. Neurochem. 47:614-616(1986).
 RN [11]
 RP SEQUENCE OF 148-304 (ISOFORM 5), AND CITRULLINATION OF C8.
 RC TISSUE=Brain;
 RX MEDLINE=89174797; PubMed=2466844;
 RA Wood D.D., Moscarello M.A.;
 RC "The isolation, characterization, and lipid-aggregating properties of
 RA a citrulline containing myelin basic protein.";
 RL J. Biol. Chem. 264:5121-5127(1989).
 RN [12]
 RP SEQUENCE OF 179-223 (ISOFORM 5), AND MASS SPECTROMETRY.
 RX MEDLINE=84185608; PubMed=6201481;
 RA Gibson B.W., Gilliom R.D., Whitaker J.N., Biemann K.;
 RC "Amino acid sequence of human myelin basic protein peptide 45-89 as
 RA determined by mass spectrometry.";
 RL J. Biol. Chem. 259:5028-5031(1984).
 RN [13]
 RP SEQUENCE OF 246-269 (ISOFORM 3), AND ENCEPHALITOGENIC PEPTIDE.
 RX MEDLINE=71088405; PubMed=4099924;
 RA Lennon V.A., Wilks A.V., Carnegie P.R.;
 RC "Immunologic properties of the main encephalitogenic peptide from the
 RA basic protein of human myelin.";
 RL J. Immunol. 105:1223-1230(1970).
 RN [14]
 RP SEQUENCE OF 156-172 AND 302-304, AND CHARACTERIZATION OF C8.
 RC TISSUE=Brain;
 RX MEDLINE=96004793; PubMed=7574672;
 RA Boulias C., Pang H., Mastronardi F., Moscarello M.A.;
 RC "The isolation and characterization of four myelin basic proteins from
 RA the unbound fraction during CM52 chromatography.";
 RL Arch. Biochem. Biophys. 322:174-182(1995).
 RN [15]
 RP METHYLATION.
 RX MEDLINE=72066401; PubMed=5128665;
 RA Baldwin G.S., Carnegie P.R.;
 RC "Isolation and partial characterization of methylated arginines from
 RA the encephalitogenic basic protein of myelin.";
 RL Biochem. J. 123:69-74(1971).
 RN [16]
 RP STRUCTURE OF 135-148 BY NMR.

Query Match 100.0%; Score 260; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. No. 2.5e-25;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYSLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
 DB 195 HHPARTAHYSLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 240

RESULT 2

MBP_PANTR MBP_PANTR STANDARD; PRT; 171 AA.
 AC P06906;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Myelin basic protein (MBP).
 GN MBP.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP PRELIMINARY SEQUENCE.
 RX MEDLINE=76009821; PubMed=51459;
 RA Westall F.C., Thompson M., Kaiter S.S.;
 RT "The proposed sequence of the encephalitogenic protein from
 chimpanzee brain.";
 RL Life Sci. 17:219-223(1975).
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
 myelin membrane in the CNS. Has a role in both the formation and
 stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 CC function in the assembly of an optimized, biochemically functional
 CC myelin membrane (By similarity).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -1- PTM: As in other animals, several charge isomers may be produced
 CC as a result of optional posttranslational modifications, such as
 CC phosphorylation of serine or threonine residues, deamidation of
 CC glutamine or asparagine residues, citrullination and methylation
 CC of arginine residues.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 DR PIR; A03139; MRC2B.
 DR HSP; P02686; IQCL.
 DR InterPro; IPR000548; Myelin_BP.
 DR Pfam; PF01669; Myelin_MBP; 1.
 DR PRINTS; PR00212; MYELINBP.
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Citrullination; Autoimmune encephalomyelitis.
 FT MOD_RES 1 1 ACETYLATION.
 FT MOD_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY
 FT MOD_RES 7 7 SIMILARITY).
 FT MOD_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 56 56 PHOSPHORYLATION (PARTIAL) (BY
 FT MOD_RES 56 56 SIMILARITY).
 FT MOD_RES 98 98 PHOSPHORYLATION (PARTIAL) (BY
 FT MOD_RES 98 98 SIMILARITY).
 FT MOD_RES 103 103 DEAMIDATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 107 107 METHYLATION (MONO-OR DI-) (BY
 FT MOD_RES 107 107 SIMILARITY).
 FT MOD_RES 115 115 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 122 122 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 130 130 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 148 148 DEAMIDATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 160 160 CITRULLINATION (PARTIAL) (BY
 FT MOD_RES 162 162 SIMILARITY).
 FT MOD_RES 166 166 PHOSPHORYLATION (PARTIAL) (BY
 FT MOD_RES 166 166 SIMILARITY).

FT MOD_RES 171 171 CITRULLINATION (BY SIMILARITY).
 SQ SEQUENCE 171 AA; 18560 MW; E5FED59DE6933293 CRC64;

Query Match 93.1%; Score 242; DB 1; Length 171;
 Best Local Similarity 95.7%; Pred. No. 2.4e-23;
 Matches 44; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHPARTAHYSLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 46
 DB 61 HHPARTAHYSLPQKSHGRGTQDENPVVHFFKNIVTPTPTPPSQGK 106

RESULT 3

MBP_PIG MBP_PIG STANDARD; PRT; 171 AA.
 ID P81558; P98189;
 AC P81558; P98189; (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Myelin basic protein (MBP).
 GN MBP.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE, AND METHYLATION OF ARG-107.
 RX TISSUE=Brain;
 RX MEDLINE=85056964; PubMed=2578056;
 RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;
 RT "Amino acid sequence of porcine myelin basic protein.";
 RL J. Neurochem. 44:134-142(1985).
 CC [2]
 CC ERRATUM.
 CC Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;
 RA J. Neurochem. 44:1663-1663(1985).
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
 CC myelin membrane in the CNS. Has a role in both the formation and
 CC stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 CC function in the assembly of an optimized, biochemically functional
 CC myelin membrane (By similarity).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -1- PTM: As in other animals, several charge isomers may be produced
 CC as a result of optional posttranslational modifications, such as
 CC phosphorylation of serine or threonine residues, deamidation of
 CC glutamine or asparagine residues, citrullination and methylation
 CC of arginine residues.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 DR HSP; P02686; IQCL.
 DR InterPro; IPR000548; Myelin_BP.
 DR Pfam; PF01669; Myelin_MBP; 1.
 DR PRINTS; PR00212; MYELINBP.
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Citrullination.
 FT MOD_RES 1 1 ACETYLATION.
 FT MOD_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY
 FT MOD_RES 7 7 SIMILARITY).
 FT MOD_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 55 55 PHOSPHORYLATION (PARTIAL) (BY
 FT MOD_RES 55 55 SIMILARITY).
 FT MOD_RES 98 98 PHOSPHORYLATION (PARTIAL) (BY
 FT MOD_RES 98 98 SIMILARITY).
 FT MOD_RES 103 103 DEAMIDATION (MONO-OR DI-).
 FT MOD_RES 107 107 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 115 115 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 130 130 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 148 148 DEAMIDATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 160 160 CITRULLINATION (PARTIAL) (BY SIMILARITY).

Db 61 HHAARTTHYGSLPOKSO-RSQDENPVVHFKNIVTRTPPPSQGK 105

RESULT 6

MBP_MOUSE

ID MBP_MOUSE

AC P04370; Q03139; Q01585; Q03176; Q9QW1; Q99KE4; Q61836; Q61837;

DT 20-MAR-1987 (Rel. 04, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Myelin basic protein (MBP) (Myelin A1 protein).

GN MBP OR SHI

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=93186801; PubMed=7680345;

RA Campagnoni A.T., Pribyl T.M., Campagnoni C.W., Kampf K.,

RA Anur-Umarjee S., Landry C.F., Handley V.W., Newman S., Garbay B.,

RA Kitamura K.;

RT "Structure and developmental regulation of Golli-mbp, a 105-kilobase

RT gene that encompasses the myelin basic protein gene and is expressed

RT in cells in the oligodendrocyte lineage in the brain.";

RL J. Biol. Chem. 268:4930-4938(1993).

RN [2]

RN SEQUENCE FROM N.A. (ISOFORM 2).

RC STRAIN=C57BL/6; TISSUE=Bone marrow;

RX MEDLINE=93057537; PubMed=1279125;

RA Grima B., Zelenika D., Pessac B.;

RT "A novel transcript overlapping the myelin basic protein gene.";

RL J. Neurochem. 59:2318-2323(1992).

RN [3]

RN SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 8).

RC MEDLINE=86079555; PubMed=2416470;

RA de Ferra F., Engh H., Hudson L., Kamholz J., Puckett C., Molineaux S.,

RA Lazzarini R.A.;

RT "Alternative splicing accounts for the four forms of myelin basic

RT protein.";

RL Cell 43:721-727(1985).

RN [4]

RN SEQUENCE FROM N.A. (ISOFORM 5).

RC MEDLINE=85254913; PubMed=2410136;

RA Takahashi N., Roach A., Teplow D.B., Prusiner S.B., Hood L.E.;

RT "Cloning and characterization of the myelin basic protein gene from

RT mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate

RT use of exons.";

RL Cell 42:139-148(1985).

RN [5]

RN SEQUENCE FROM N.A. (ISOFORM 6), AND SEQUENCE OF 9-194 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=87118269; PubMed=2433693;

RA Newman S., Kitamura K., Campagnoni A.T.;

RT "Identification of a cDNA coding for a fifth form of myelin basic

RT protein in mouse.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).

RN [6]

RN SEQUENCE FROM N.A. (ISOFORM 8).

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [7]

RN SEQUENCE FROM N.A. (ISOFORM 9).

RC TISSUE=Breast tumor;

RX Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RN [8]

RN SEQUENCE OF 135-157 FROM N.A.

RC MEDLINE=8252919; PubMed=2470651;

RA Miura M., Tamura T.A., Aoyama A., Mikoshiba K.;

RT "The promoter elements of the mouse myelin basic protein gene

RT function efficiently in NG108-15 neuronal/gial cells.";

RL Gene 75:31-38(1989).

RN [9]

RN PARTIAL SEQUENCE FROM N.A. (25 AA INSERTION OF ISOFORMS 4; 6 AND 9).

RC MEDLINE=86259714; PubMed=2425357;

RA Kamholz J., de Ferra F., Puckett C., Lazzarini R.A.;

RT "Identification of three forms of human myelin basic protein by cDNA

RT cloning.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).

RN [10]

RN SEQUENCE OF 193-222 FROM N.A.

RC MEDLINE=84119431; PubMed=6198644;

RA Zeller N.K., Hunkeler M.J., Campagnoni A.T., Sprague J.,

RA Lazzarini R.A.;

RT "Characterization of mouse myelin basic protein messenger RNAs with a

RT myelin basic protein cDNA clone.";

RL Proc. Natl. Acad. Sci. U.S.A. 81:18-22(1984).

RN [11]

RN PARTIAL SEQUENCE FROM N.A. (22 AA INSERTION OF ISOFORMS 10 AND 11).

RC TISSUE=spinal cord;

RX MEDLINE=91162193; PubMed=1705957;

RA Aruga J., Okano H., Mikoshiba K.;

RT "Identification of the new isoforms of mouse myelin basic protein: the

RT existence of exon 5a.";

RL J. Neurochem. 56:1222-1226(1991).

RN [12]

RN PARTIAL SEQUENCE FROM N.A. (ISOFORMS 12; 13 AND 14).

RC MEDLINE=93203893; PubMed=7681106;

RA Nakajima K., Ikenaka K., Kagawa T., Aruga J., Nakao J., Nakahira K.,

RA Shiota C., Kim S.U., Mikoshiba K.;

RT "Novel isoforms of mouse myelin basic protein predominantly expressed

RT in embryonic stage.";

RL J. Neurochem. 60:1554-1563(1993).

RN [13]

RN SEQUENCE OF 191-224 FROM N.A.

RC MEDLINE=88196094; PubMed=2452084;

RA Okano H., Tamura T., Miura M., Aoyama A., Ikenaka K., Oshimura M.,

RA Mikoshiba K.;

RT "Gene organization and transcription of duplicated MBP genes of myelin

RT deficient (shi(mld)) mutant mouse.";

RL EMBO J. 7:77-83(1988).

RN [14]

RN DEVELOPMENTAL STAGE.

RC MEDLINE=98409779; PubMed=9736652;

RA Landry C.F., Pribyl T.M., Ellison J.A., Givogri M.I., Kampf K.,

RA Campagnoni C.W., Campagnoni A.T.;

RT "Embryonic expression of the myelin basic protein gene: identification

RT of a promoter region that targets transgene expression to pioneer

RT neurons.";

RL J. Neurosci. 18:7315-7327(1998).

RN [15]

RN FUNCTION.

RC MEDLINE=21018209; PubMed=11145205;


```

RESULT 9
MBP_CHICK STANDARD; PRT; 173 AA.
AC PI5720;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Myelin basic protein (MBP).
GN MBP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=White leghorn; Tissue=Optic lobe;
RA MEDLINE=89358239; PubMed=2475444;
RX Zopf D., Sonntag H., Betz H., Gundelfinger E.D.;
RT "Developmental accumulation and heterogeneity of myelin basic protein
transcripts in the chick visual system.";
RL Glia 2:241-249(1989).
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
myelin membrane in the CNS. Has a role in both the formation and
stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
function in the assembly of an optimized, biochemically functional
myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (major form) (shown
here) and 2: are produced by alternative splicing.
CC -1- DEVELOPMENTAL STAGE: In the optic lobe, first detected at
embryonic day 14. Expression strongly increases between embryonic
days 16 and 18, reaches a maximum at postnatal day 1, and then
declines again to the adult level.
CC -1- PTM: As in other animals, several charge isomers may be produced
as a result of optional posttranslational modifications, such as
phosphorylation of serine or threonine residues, deamidation of
glutamine or asparagine residues, citrullination and methylation
of arginine residues.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
-----
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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DR EMBL: X17103; CAA34959.1; -
DR PIR: S08535; S08535.
DR HSP: P02686; 1OCL.
DR InterPro: IPR000548; Myelin_BP.
DR Pfam: PF01669; Myelin_MBP; 1.
DR PRINTS: PR00212; MYELINMBP.
DR PROSITE: PS00569; MYELIN_MBP; 1.
KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
Citrullination; Alternative splicing.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT MOD_RES 24 24 CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 29 29 CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 96 96 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT MOD_RES 101 101 DEAMIDATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 105 105 METHYLATION (MONO-OR DI-) (BY
FT SIMILARITY).
FT MOD_RES 113 113 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 146 146 DEAMIDATION (PARTIAL) (BY SIMILARITY).
-----
FT MOD_RES 164 164 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT MOD_RES 168 168 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT MOD_RES 173 173 CITRULLINATION (BY SIMILARITY).
FT VARSPLIC 104 114 MISSING (IN ISOFORM 2).
SQ SEQUENCE 173 AA; 18677 MW; ABFE70D4C9CF019D CRC64;

Query Match 69.8%; Score 181.5; DB 1; Length 173;
Best Local Similarity 71.7%; Pred. No. 8.7e-16;
Matches 33; Conservative 5; Mismatches 1; Gaps 1;

OY 2 HPARTAHYGLSPQKS-HGRTODENPVVHFFKNIIVTRTPPPSQGK 46
| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 59 HAARASHVGSIPORSQGRGDDNPVHFFKNIIVSRTPPPMQAKG 104
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
MBP_XENLA STANDARD; PRT; 175 AA.
AC P87346;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin basic protein (MBP) (Myelin A1 protein).
GN MBP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J; Tissue=Brain;
RA Negata S., Ogino K.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
myelin membrane in the CNS. Have a role in both the formation and
stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
function in the assembly of an optimized, biochemically functional
myelin membrane (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -1- PTM: As in other animals, several charge isomers may be produced
as a result of optional posttranslational modifications, such as
phosphorylation of serine or threonine residues, deamidation of
glutamine or asparagine residues, citrullination and methylation
of arginine residues.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
-----
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or send an email to license@isb-sib.ch).
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DR EMBL: AB000736; BAA19174.1; -
DR HSP: P02686; 1OCL.
DR InterPro: IPR000548; Myelin_BP.
DR Pfam: PF01669; Myelin_MBP; 1.
DR PRINTS: PR00212; MYELINMBP.
KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
Citrullination.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 6 6 PHOSPHORYLATION (PARTIAL) (BY
FT SIMILARITY).
FT MOD_RES 24 24 CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT MOD_RES 32 32 CITRULLINATION (PARTIAL) (BY SIMILARITY).

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Query Match          31.2%; Score 81; DB 1; Length 154;
Best Local Similarity 43.2%; Pred. No. 0.0028;
Matches 16; Conservative 7; Mismatches 8; Indels 6; Gaps 1;

QY 7 AHYGLSPQKSHGRQTQDENPVVHFKNIVPTPTPPSQ 43
   || | : | : ||| ||| : | : |
Db 61 AHQGA-----RRQTDDSPVHFKNMSPKAPVQ 91

RESULT 12
MBP_SQAC
ID MBP_SQAC STANDARD; PRT; 154 AA.
AC Q91439;
DC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Myelin basic protein (MBP).
GN MBP.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and spinal cord;
RX MEDLINE=94016687; PubMed=7692075;
RA Spivack W.D., Zhong N., Salerno S., Saavedra R.A., Gould R.M.;
RT "Molecular cloning of the myelin basic proteins in the shark, Squalus
RT acanthias, and the ray, Raja erinacea."
RL J. Neurosci. Res. 35:577-584(1993).
CC I- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
CC OF MYELIN.
CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -I- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
-----
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-----
EMBL: U44052; AAA96757.1; -
HSSP: P02866; IQCLL.
InterPro: IPR000548; Myelin_BP.
Pfam: PF01669; Myelin_MBP; 1.
PRINTS: PR00212; MYELINMBP.
PROSITE: PS00569; MYELIN_MBP; 1.
Myelin: Structural protein; Acetylation; Phosphorylation.
INIT_MET 0 0 BY SIMILARITY.
MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
SEQUENCE 154 AA; 16479 MW; C129F8A824ABBC93 CRC64;

Query Match          31.2%; Score 81; DB 1; Length 154;
Best Local Similarity 43.2%; Pred. No. 0.0028;
Matches 16; Conservative 7; Mismatches 8; Indels 6; Gaps 1;

QY 7 AHYGLSPQKSHGRQTQDENPVVHFKNIVPTPTPPSQ 43
   || | : | : ||| ||| : | : |
Db 61 AHQGA-----RRQTDDSPVHFKNMSPKAPVQ 91

RESULT 13
MBP_HETFR
ID MBP_HETFR STANDARD; PRT; 154 AA.
AC P20939;
DC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

```

DE Myelin basic protein (MBP).
GN MBP.
OS Heterodontus francisci (Horn shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Heterodontidae; Heterodontiformes;
OC Heterodontidae; Heterodontus.
OX NCBI_TaxID=7792;
RN [1]
RP SEQUENCE FROM N.A.
RC TTSUE=Brain;
RX MEDLINE=90040744; PubMed=2478717;
RA Saavedra R.A., Fors L., Aebersold R.H., Arden B., Horvath S.,
RA Sanders J., Hood L.;
RT "The myelin proteins of the shark brain are similar to the myelin
RT proteins of the mammalian peripheral nervous system.";
RL J. Mol. Evol. 29:149-156(1989).
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
CC OF MYELIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X17664; CAA35661.1; -;
CC PIR: B32999; B32999.
CC HSP: P02686; I0CL.
CC InterPro: IPR000548; Myelin_BP.
CC Pfam: PF01669; Myelin_MBP.1.
CC PRINTS: PR00212; MYELINMBP.
CC PROSITE: PS00569; MYELIN_MBP; 1.
CC MYELIN: Structural protein; Acetylation; Phosphorylation.
CC INIT_MET 0 BY SIMILARITY.
CC MOD_RES 1 ACETYLATION (BY SIMILARITY).
CC SEQUENCE 154 AA; 16502 MW; A9A57DA149429A83 CRC64;

Query Match 31.0%; Score 80.5; DB 1; Length 154;
Best Local Similarity 41.9%; Pred. No. 0.0032;
Matches 18; Conservative 7; Mismatches 9; Indels 9; Gaps 2;

QY 4 ARTAHYSLPQKSH---GRQDENPVVHFKNIVTPRTPPSQ 43
DB 55 APTTH-----KAHQAAGRTQDSDAVVHFKNMSPKKAPVQ 91

RESULT 14
ID OAF_DROME STANDARD; PRT; 487 AA.
AC Q9NLA6; Q24556;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Out at first protein (Contains: Out at first short protein).
GN OAF OR CG9884.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BERKELEY; TISSUE=Embryo;
RX MEDLINE=95286060; PubMed=7768442;
RA Bergstrom D.E., Merli C.A., Cygan J.A., Shelby R., Blackman R.K.;
RT "Regulatory autonomy and molecular characterization of the Drosophila
RT out at first gene.";
RL Genetics 139:1331-1346(1995).

RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Prankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Gerhart W.M., Glasser K.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Wellsteinbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 1-89 FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=OREGON-R;
RX MEDLINE=96217926; PubMed=8675012;
RA Merli C., Bergstrom D.E., Cygan J.A., Blackman R.K.;
RT "Promoter specificity mediates the independent regulation of
RT neighboring genes.";
RL Genes Dev. 10:1260-1270(1996).
CC -1- FUNCTION: VITAL FOR PROPER NEURONAL DEVELOPMENT AND HATCHING.
CC -1- TISSUE SPECIFICITY: EMBRYONIC EXPRESSION IS IN SMALL CLUSTERS OF
CC CELLS ALONG POSTERIOR MARGIN OF MOST SEGMENTS, BRAIN AND
CC SEGMENTALLY REPEATING PATTERN ALONG MIDLIN OF NERVE CORD
CC EXPRESSED IN EMBRYONIC, LARVAL AND ADULT GONADS OF BOTH SEXES, AND
CC LARVAL IMAGINAL DISKS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY
CC THROUGHOUT DEVELOPMENT WITH HIGHEST LEVELS IN PUPAE AND ADULTS.
CC -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UGA MAY OCCUR BETWEEN
CC THE CODONS FOR 332-GLU AND 334-ARG.
CC -----
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CC -----
CC EMBL: L31349; AAC37219.2; -;
CC EMBL: AE003583; AAF51246.1; ALT_TERM.
CC EMBL: U63852; AAC47551.1; -;
CC FlyBase; FBgn0011818; oaf.

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OK protein - protein search, using sw model

Run on: August 28, 2002, 16:35:08 ; Search time 41.39 Seconds
(without alignments)
192.263 Million cell updates/sec

Title: US-09-813-383-1
Perfect score: 260
Sequence: 1 HHPATAHYGSLPKSHGRT.....VHEFKNIVTPPPPSOGKG 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
|------------|-------|-------|--------|----|---------------------|
| 1 | 78.5 | 30.2 | 128 | 13 | P98190 carcharhinu |
| 2 | 64.5 | 24.8 | 448 | 13 | O93382 gallus gall |
| 3 | 63 | 24.2 | 632 | 16 | O91250 pseudomonas |
| 4 | 62 | 23.8 | 709 | 5 | O9V089 drosophila |
| 5 | 60.5 | 23.3 | 1723 | 4 | O92576 homo sapien |
| 6 | 60.5 | 23.3 | 1957 | 4 | O9NQ16 homo sapien |
| 7 | 60.5 | 23.3 | 2039 | 4 | O9UI45 homo sapien |
| 8 | 60 | 23.1 | 676 | 5 | O95WV0 drosophila |
| 9 | 60 | 23.1 | 685 | 15 | O9YWM3 gibbon ape |
| 10 | 59.5 | 22.9 | 2556 | 11 | O91XW2 mus musculus |
| 11 | 59 | 22.7 | 238 | 2 | O9AES0 pasteurilla |
| 12 | 59 | 22.7 | 248 | 10 | O9ASD4 oryza sativ |
| 13 | 59 | 22.7 | 401 | 5 | O965J5 caenorhabdi |
| 14 | 59 | 22.7 | 441 | 5 | O27378 caenorhabdi |
| 15 | 59 | 22.7 | 556 | 16 | O9JVG1 neisseria m |
| 16 | 59 | 22.7 | 608 | 16 | O9K0G2 neisseria m |

| | | | | | |
|----|------|------|------|----|--------|
| 17 | 59 | 22.7 | 625 | 2 | O9R9E7 |
| 18 | 59 | 22.7 | 736 | 10 | O23362 |
| 19 | 59 | 22.7 | 1160 | 12 | O86928 |
| 20 | 59 | 22.7 | 1514 | 4 | O9H0B0 |
| 21 | 59 | 22.7 | 1564 | 4 | O96JN8 |
| 22 | 58.5 | 22.5 | 607 | 5 | O9V925 |
| 23 | 58.5 | 22.5 | 607 | 5 | O960E4 |
| 24 | 57.5 | 22.1 | 266 | 12 | O56868 |
| 25 | 57 | 21.9 | 137 | 6 | O9BDE4 |
| 26 | 56.5 | 21.7 | 363 | 16 | O9A0Q7 |
| 27 | 56.5 | 21.7 | 444 | 11 | O62219 |
| 28 | 56.5 | 21.7 | 462 | 12 | O40938 |
| 29 | 56.5 | 21.7 | 760 | 13 | O9DDU6 |
| 30 | 56.5 | 21.7 | 2228 | 10 | O48579 |
| 31 | 56 | 21.5 | 235 | 2 | O9X528 |
| 32 | 56 | 21.5 | 562 | 5 | O22068 |
| 33 | 56 | 21.5 | 564 | 5 | O952Q4 |
| 34 | 55 | 21.3 | 943 | 5 | O9V0F3 |
| 35 | 55.5 | 21.3 | 973 | 4 | O9P203 |
| 36 | 55.5 | 21.3 | 973 | 4 | O9P203 |
| 37 | 55 | 21.2 | 257 | 16 | O9KVD6 |
| 38 | 55 | 21.2 | 262 | 4 | O9UJ34 |
| 39 | 55 | 21.2 | 422 | 10 | O23764 |
| 40 | 55 | 21.2 | 579 | 4 | O9H7K3 |
| 41 | 55 | 21.2 | 732 | 5 | O960C3 |
| 42 | 55 | 21.2 | 891 | 16 | O9PAG7 |
| 43 | 55 | 21.2 | 1016 | 4 | O9BR83 |
| 44 | 55 | 21.2 | 1184 | 4 | O96S08 |
| 45 | 55 | 21.2 | 1751 | 5 | O17143 |

ALIGNMENTS

RESULT 1

| | | | | | |
|--------|---|---|--------------|------|---------|
| P98190 | ID | P98190 | PRELIMINARY; | PRT; | 128 AA. |
| AC | P98190; | | | | |
| DT | 01-MAY-2000 | (TReMBLrel. 13, Created) | | | |
| DT | 01-MAY-2000 | (TReMBLrel. 13, Last sequence update) | | | |
| DT | 01-JUN-2001 | (TReMBLrel. 17, Last annotation update) | | | |
| DE | MYELIN BASIC PROTEIN (MBP) | (FRAGMENTS). | | | |
| OS | Carcharhinus obscurus | (Dusky shark). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; | | | | |
| OC | Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; | | | | |
| OC | Carcharhinidae; Carcharhinus. | | | | |
| OX | NCBI_TaxID=7807; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE. | | | | |
| RC | TISSUE-BRAIN; | | | | |
| RX | MEDLINE-90347482; PubMed-1696624; | | | | |
| RA | Milne T.J., Atkins A.R., Warren J.A., Auton W.P., Smith R.; | | | | |
| RT | "Shark myelin basic protein: amino acid sequence, secondary structure, and self-association." | | | | |
| RT | J. Neurochem. 55:950-955(1990). | | | | |
| RL | - FUNCTION: CONSTITUTES WITH LIPOPHILLIN THE MAJOR PROTEINS OF MYELIN IN THE CNS (85% OF THE TOTAL MEMBRANE PROTEINS). ASSOCIATES PRIMARILY WITH ACIDIC LIPIDS. FLUIDIZES THE BILAYER AND ALTERS ITS PERMEABILITY. INDUCES THE FORMATION OF A COMPACT MULTILAYER ARRANGEMENT OF BILAYERS (BY SIMILARITY). | | | | |
| CC | - SUBUNIT: SELF-ASSOCIATES IN THE PRESENCE OF LYSOLIPID (BY SIMILARITY). | | | | |
| CC | - SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN. | | | | |
| CC | - PTM: THE N-TERMINUS IS BLOCKED (PROBABLE). | | | | |
| DR | HSPSP: P02686; I0CL. | | | | |
| DR | InterPro: IPR000548; Myelin_BP. | | | | |
| DR | Pfam: PF01669; Myelin_MBP; 1. | | | | |
| KW | PROSITE: PS00569; MYELIN_MBP; 1. | | | | |
| DR | Myelin; Structural protein; Phosphorylation. | | | | |
| FT | NON_TER | 1 | 1 | | |
| FT | NON_CONS | 5 | 6 | | |
| FT | MOD_RES | 55 | 55 | | |
| FT | MOD_RES | 65 | 65 | | |

DEAMIDATION (PARTIAL) (BY SIMILARITY).
DEAMIDATION (PARTIAL) (BY SIMILARITY).

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FT MOD_RES 124 124 PHOSPHORYLATION (PARTIAL)
FT MOD_RES 128 128 (BY SIMILARITY)
FT CITRULLINATION (BY SIMILARITY)
SQ SEQUENCE 128 AA: 13747 MW: 104E952B794A4D79 CRC64,

Query Match 30.2%; Score 78.5; DB 13; Length 128;
Best Local Similarity 43.6%; Pred. No. 0.0083;
Matches 17; Conservative 7; Mismatches 6; Indels 9; Gaps 2;

QY 4 ARTAHYGLSPQKSH---GRQDENPVVHFFKNIVTPRTP 39
   | | | | | | | | | | | | | | | | | | | | |
Db 30 APTLH-----KAHQAGRTDDSAVVHFFKNMSPKAP 62
   | | | | | | | | | | | | | | | | | | | | |

RESULT 2
ID O93382 PRELIMINARY; PRT; 448 AA.
AC O93382;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RAB-GDP DISSOCIATION INHIBITOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CILIARY GANGLION;
EX MEDLINE=9836372; PubMed=9698324;
RA Kononov O.C., Kulesa M.C., Shisheva A.C., Jacob M.H.;
RT "Innovation and target tissue interactions induce Rab-GDP
RT dissociation inhibitor (GDI) expression during peripheral synapse
RT formation in developing chick ciliary ganglion neurons in situ.";
RL J. Neurosci. 18:6331-6339(1998).
DR EMBL: AF076291; AAC31910.1;
DR HSP: P21856; IGDND.
DR InterPro: IPR002005; Rab_GDI_REP.
DR Pfam: PF00996; GDI; 1.
DR PRINTS: PR00891; RABGDIREP.
SQ SEQUENCE 448 AA: 50683 MW: 87F93A96CCD51F83 CRC64;

Query Match 24.8%; Score 64.5; DB 13; Length 448;
Best Local Similarity 31.1%; Pred. No. 2.4;
Matches 14; Conservative 6; Mismatches 18; Indels 7; Gaps 1;

QY 2 HPARAHYGLSPQKSHGRQDENPVVHFFKNIVTPRTPPSGKG 46
   | | | | | | | | | | | | | | | | | | | | |
Db 32 HMDRNSYTG-----GESASITPLEDLYKRFNLPGTPPESMGRG 69
   | | | | | | | | | | | | | | | | | | | | |

RESULT 3
ID O91250 PRELIMINARY; PRT; 632 AA.
AC O91250;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE COPPER RESISTANCE PROTEIN A PRECURSOR.
OS PCOA OR PA2065.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
EX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

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RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.J., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004633; AAG05453.1;
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR001287; Cu-nit rdctse.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002355; MultiCu_oxidase2.
DR Pfam: PF00394; Cu-oxidase; 3.
DR PRINTS: PR00695; CUNOZRDYASE.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_1.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE: PS00080; MULTICOPPER_OXIDASE2; 1.
KW Complete proteome.
SQ SEQUENCE 632 AA: 69851 MW: 229DA2AE86F5B519 CRC64;

Query Match 24.2%; Score 63; DB 16; Length 632;
Best Local Similarity 34.3%; Pred. No. 5.7;
Matches 12; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 10 GSLPQKSHGRQDENPVVHFFKNIVTPRTPPSQG 44
   | | | | | | | | | | | | | | | | | | | | |
Db 451 GAMPQSHPSASEDGNPLVDQMTPFKLADPGLG 485
   | | | | | | | | | | | | | | | | | | | | |

RESULT 4
ID O9VU89 PRELIMINARY; PRT; 709 AA.
AC O9VU89;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CG10710 PROTEIN.
GN CG10710.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
EX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Duan A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mervilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

```

| | | |
|--------|---------|--------------|
| RESULT | 8 | |
| Q95WV0 | | |
| ID | Q95WV0 | PRELIMINARY; |
| AC | Q95WV0; | PRT; 676 AA. |

| | |
|------------------|--|
| OS | Caenorhabditis elegans. |
| OC | Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; |
| OC | Rhabditidae; Pelodierinae; Caenorhabditis. |
| NCBI_TaxID=6239; | |
| [1] | SEQUENCE FROM N.A. |
| RP | STRAIN=BRISTOL N2; |
| RC | MEDLINE=99069613; PubMed=9851916; |
| RY | None; |
| RA | "Genome sequence of the nematode C. elegans: a platform for |
| RT | investigating biology. The C. elegans Sequencing Consortium." |
| RT | Science 282:2012-2018(1998). |
| RL | [2] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=BRISTOL N2; |
| RY | Miller N., Biewald T.; |
| RA | "The sequence of C. elegans cosmid C37F5." |
| RT | Submitted (MAY-1998) to the EMBL/GenBank/DBDJ databases. |
| RL | [3] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=BRISTOL N2; |
| RY | Waterston R.; |
| RA | "Direct Submission"; |
| RT | Submitted (JUN-2001) to the EMBL/GenBank/DBDJ databases. |
| RT | EMBL; AF067606; AAC17530.2; " |
| DR | SEQUENCE 401 AA, 43630 MW; FD09c64BBA028A6D6 CRC64; |
| SO | |

| | | | | |
|-----------------------|---|--|--------|-------------|
| Query Match | 22.7% | Score 59; | DB 5; | Length 441; |
| Best Local Similarity | 31.2% | Pred. No. 13; | | |
| Matches 15; | Conservative | 7; | Indels | 20; |
| Caps | | | | |
| | | | | |
| QY | 16 | SHGRT-----QDENPVVHFFKNIVTRTP---PPSQ | 43 | |
| | | | | |
| | | | | |
| Db | 368 | SSGRTPGLGESQVFQPPVSAFQATNPLLNTFSNLIISPMAPFMMPPSQ | 415 | |
| | | | | |
| RESULT | 15 | | | |
| ID | Q9JVG1 | PRELIMINARY; | PRT; | 556 AA. |
| AC | Q9JVG1; | | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Created) | | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Last sequence update) | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last annotation update) | | | |
| GN | PUTATIVE ADHESIN. | | | |
| GE | MAFE3 OR NMA0853. | | | |
| OS | Neisseria meningitidis (serogroup A). | | | |
| OC | Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria | | | |
| OX | NCBI_TaxID=65699; | | | |
| RP | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A; | | | |
| RC | MEDLINE=20222556; PubMed=10761919; | | | |
| RA | Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., | | | |
| RA | Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., | | | |
| RA | Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., | | | |
| RA | Jagels K., Leather S., Moule S., Mungall K., Quail M.A., | | | |
| RA | Rajandream M.A., Rutherford K.M., Simmonds M., Stelton J., | | | |
| RT | Whitehead S., Spratt B.G., Barrall B.G.; | | | |
| RT | *Complete DNA sequence of a serogroup A strain of Neisseria | | | |
| RL | meningitidis Z2491.*; | | | |
| RL | Nature 404:502-506(2000). | | | |

| | | | | |
|-----------------------|-----------------|----------------|-----------|-------------|
| Query Match | 22.7% | Score 59; | DB 16; | Length 556; |
| Best Local Similarity | 35.9% | Pred. No. 17; | | |
| Matches 14; | Conservative 2; | Mismatches 23; | Indels 0; | Gaps 0; |

Qy 7 AHYGSLPQKSHGRTQDENPVWHFFKNIVTRTPPPSQGK 45
| | | | | : | | | | |
Db 363 AAYAKYPSPHYSRNIRSNLEQRYGKENITSTVPPPSNGK 401

Search completed: August 28, 2002, 16:41:23
Job time: 375 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 16:35:03 ; Search time 51.58 Seconds
(without alignments)
38.762 Million cell updates/sec

Title: US-09-813-383-1_COPY_8_25
Perfect score: 103
Sequence: 1 HYGSLPQKSHGRQDENP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802:*
1: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
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14: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
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17: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 103 | 100.0 | 41 | 20 AAY04044 | Human myelin basic |
| 2 | 103 | 100.0 | 46 | 19 AAW72360 | Human myelin basic |
| 3 | 103 | 100.0 | 170 | 15 AAR48592 | Human myelin basic |
| 4 | 103 | 100.0 | 170 | 17 AAR95406 | Myelin oligodendro |
| 5 | 103 | 100.0 | 171 | 17 AAR97627 | Human myelin basic |
| 6 | 103 | 100.0 | 171 | 17 AAR99560 | Human myelin basic |
| 7 | 103 | 100.0 | 171 | 20 AAY27284 | Human myelin basic |
| 8 | 103 | 100.0 | 171 | 21 AAB19513 | Human myelin basic |
| 9 | 103 | 100.0 | 171 | 21 AAY69394 | Amino acid sequenc |
| 10 | 103 | 100.0 | 171 | 21 AAY44234 | Human myelin basic |
| 11 | 103 | 100.0 | 186 | 21 AAY57090 | Human myelin basic |

| | | | | | |
|----|------|-------|-----|-------------|--------------------|
| 12 | 103 | 100.0 | 197 | 17 AAW00399 | Human myelin basic |
| 13 | 103 | 100.0 | 197 | 21 AAY95922 | Human myelin bindi |
| 14 | 103 | 100.0 | 203 | 17 AAW06107 | Foetal myelin basi |
| 15 | 103 | 100.0 | 203 | 17 AAW06108 | Foetal myelin basi |
| 16 | 103 | 100.0 | 373 | 17 AAW06103 | MP4 chimera (MBP21 |
| 17 | 103 | 100.0 | 375 | 17 AAW06104 | MP4 chimera (delta |
| 18 | 103 | 100.0 | 385 | 17 AAW06102 | MP3 chimera (MBP21 |
| 19 | 103 | 100.0 | 492 | 17 AAW06105 | MMOGP4 chimera (MB |
| 20 | 97 | 94.2 | 168 | 15 AAR48594 | Rabbit myelin basi |
| 21 | 95 | 92.2 | 170 | 14 AAR35440 | Human basic myelin |
| 22 | 85 | 82.5 | 168 | 11 AAR04717 | Empirically determ |
| 23 | 85 | 82.5 | 170 | 14 AAR30736 | Human MBP. Synthe |
| 24 | 83.5 | 81.1 | 169 | 15 AAR48593 | Cattle myelin basi |
| 25 | 82 | 79.6 | 15 | 17 AAR91926 | Peptide comprising |
| 26 | 82 | 79.6 | 15 | 19 AAW72363 | Human myelin basic |
| 27 | 82 | 79.6 | 20 | 17 AAR95391 | Residues 71-90 of |
| 28 | 82 | 79.6 | 20 | 18 AAW44063 | Human myelin basic |
| 29 | 82 | 79.6 | 40 | 21 AAB12612 | Human myelin basic |
| 30 | 82 | 79.6 | 40 | 21 AAY85559 | Human MBP peptide |
| 31 | 78.5 | 76.2 | 127 | 15 AAR48596 | Rat myelin basic p |
| 32 | 78 | 75.7 | 39 | 21 AAY85561 | Human MBP peptide |
| 33 | 75.5 | 73.3 | 170 | 11 AAR02226 | Myelin basic prote |
| 34 | 75.5 | 73.3 | 170 | 14 AAR30735 | Bovine MBP. Synth |
| 35 | 75.5 | 73.3 | 170 | 15 AAR45947 | Myelin basic prote |
| 36 | 75.5 | 73.3 | 170 | 17 AAR86422 | Myelin basic prote |
| 37 | 75.5 | 73.3 | 170 | 19 AAW57236 | Myelin basic prote |
| 38 | 75.5 | 73.3 | 170 | 21 AAY58368 | Mammalian generic |
| 39 | 74 | 71.8 | 20 | 17 AAR95350 | Residues 61-80 of |
| 40 | 74 | 71.8 | 20 | 18 AAW44062 | Human myelin basic |
| 41 | 74 | 71.8 | 20 | 20 AAW73615 | Human myelin basic |
| 42 | 74 | 71.8 | 20 | 21 AAB12624 | Human myelin basic |
| 43 | 74 | 71.8 | 20 | 21 AAY85556 | Human MBP peptide |
| 44 | 67 | 65.0 | 20 | 19 AAW78824 | Myelin basic prote |
| 45 | 67 | 65.0 | 20 | 21 AAB33636 | MHC class II assoc |

ALIGNMENTS

RESULT 1

AAV04044
ID AAY04044 standard; peptide: 41 AA.

XX AC AAY04044;

XX DT 20-DEC-1999 (first entry)

XX DE Human myelin basic protein residues 60-100.

XX DE Multiple sclerosis; MS; demyelinating disease; treatment; diagnosis;
KW antigen; myelin basic protein; MBP; antibody; epitope.

XX OS Homo sapiens.

XX PN CA2201274-A.

XX PD 27-SEP-1998.

XX PF 27-NAR-1997; 97CA-2201274.

XX PR 27-NAR-1997; 97CA-2201274.

XX PA (UYBR-) UNIV BRITISH COLUMBIA.

XX PI McGeer PL, Lee G, McGeer EG;

XX DR WPI; 1999-591471/51.

XX PT Treating multiple sclerosis by administering specific peptides. -

XX PS Disclosure; Page 15; 18pp; English.

XX CC A new method is disclosed for treating multiple sclerosis and other

CC demyelinating diseases in humans. The method comprises administering
 CC a combination of peptides of less than 15 amino acids, designed to
 CC neutralize the antigenic effects of exposed epitopes in degenerating
 CC myelin. The epitopes are identified using immunohistochemical analysis
 CC of affected tissue with prepared antibodies. The peptides are mimics
 CC which block autoantibodies, and complementary or binding peptides to
 CC block the exposed antigenic epitopes. Preferably the exposed epitope
 CC on degenerating myelin is QDENPVV and the peptide to be administered
 CC is (a) QDENPVV, (b) QDENPVV-dv, (c) R1-QDENPVV-R2, (d) DYGVFIL, (e)
 CC db-DGVFI-dl or (f) R1-DYGVFIL-R2; where R1 and R2 are peptides of 1-4
 CC amino acid residues. The peptide QDENPVV corresponds to human myelin
 CC basic protein residues 82-88, and the peptide DYGVFIL is a complementary
 CC peptide to QDENPVV, i.e. it is encoded by the cDNA strand complementary
 CC to that which codes for QDENPVV. The invention also extends to a
 CC method for diagnostic differentiation between normal and degenerating
 CC myelin, using antibodies that recognize the sequence QDENPVV.

XX Sequence 41 AA;

Query Match 100.0%; Score 103; DB 20; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGSLPQKSHGRTQDENP 18
 |||||
 Db 10 hygslpqkshgrrtqdenp 27

RESULT 2

AAW72360
 ID AAW72360 standard; peptide; 46 AA.

XX AC AAW72360;

XX 16-DEC-1998 (first entry)

XX Human myelin basic protein fragment.

XX Human; myelin basic protein; MBP; multiple sclerosis; anti-MBP; MS.

XX Homo sapiens.

XX WO9845327-A1.

XX 15-OCT-1998.

XX 03-APR-1998; 98WO-CA00290.

XX 04-APR-1997; 97CA-2201841.

XX (UYAL-) UNIV ALBERTA.

XX Catz I, Warren KG;

XX WPI; 1998-568336/48.

XX Peptide and its derivatives for treatment of multiple sclerosis - is
 PT capable of neutralising or modulating production of anti-myelin
 PT basic protein

XX Disclosure; Page 15; 75pp; English.

XX The present sequence represents a myelin basic protein (MBP) protein
 CC fragment used to produce MBP peptides. MBP peptides are capable of
 CC neutralising or modulating the production of anti-myelin basic protein.
 CC The present invention also describes a method for treating multiple
 CC sclerosis (MS). The method comprises administering to the patient an
 CC MBP peptide of the formula: R1-Val-His-Phe-Phe-Lys-Asn-Ile-R2 where R1,
 CC R2 = H, OH, or an amino acid residue and a polypeptide residue,
 CC provided that R1 and R2 are not both H or OH at the same time.

XX Sequence 46 AA;

Query Match 100.0%; Score 103; DB 19; Length 46;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGSLPQKSHGRTQDENP 18
 |||||
 Db 8 hygslpqkshgrrtqdenp 25

RESULT 3

AAAR48592
 ID AAR48592 standard; protein; 170 AA.

XX AC AAR48592;

XX 31-JUL-1994 (first entry)

XX Human myelin basic protein.

XX Proteolipid protein; myelin basic protein; retrovirus;

XX neurological disease; by-stander antigen; TGF-beta;

XX transforming growth factor-beta; T-cell; T-lymphocyte;

XX myelopathy; paraparesis; human immunodeficiency virus type 1.

XX Homo sapiens.

XX WO9404121-A.

XX 03-MAR-1994.

XX 17-AUG-1993; 93WO-US07786.

XX 17-AUG-1992; 92US-0931217.

XX (AUTO-) AUTOIMMUNE INC.

XX Hafner DA, Weiner HL;

XX WPI; 1994-082786/10.

XX Treating retroviral associated neurological disease - by admin.
 PT of by-stander antigen, causing release of transforming growth
 PT factor beta from suppressor T cells

XX Disclosure; Page 49; 64pp; English.

XX Myelin basic proteins (sequences AAR48592-96) and cattle proteolipid
 CC protein (AAR48592) elicit the release of TGF-beta from suppressor T-
 CC cells and target the T-cells to neural tissue under cytotoxic
 CC attack, thereby reducing neurological disease, e.g. HTLV-1
 CC associated myelopathy, tropical spastic paraparesis and HIV
 CC infection.

XX Sequence 170 AA;

Query Match 100.0%; Score 103; DB 15; Length 170;
 Best Local Similarity 100.0%; Pred. No. 7.6e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGSLPQKSHGRTQDENP 18
 |||||
 Db 68 hygslpqkshgrrtqdenp 85

RESULT 4

AAR95406
 ID AAR95406 standard; Protein; 170 AA.

XX AC AAR95406;

XX

DT 16-DEC-1996 (first entry)
 XX Myelin oligodendrocyte protein.
 XX
 XX Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CM4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 XX
 OS Homo sapiens.
 XX
 XX W09612737-A2.
 PN
 XX
 XX 02-MAY-1996.
 PD
 XX
 XX 25-OCT-1995; 95WO-US13682.
 PF
 XX
 XX 15-MAR-1995; 95US-0404228.
 PR
 XX 25-OCT-1994; 94US-0328224.
 PR
 XX 25-OCT-1995; 95ZA-0009033.
 XX
 XX (IMMU-) IMMULOGIC PHARM CORP.
 PA
 XX Devaux B, Franzen H, Geffer M, Hsu D, Pallard X;
 PI Rothbard J, Samson M, Shi J, Smilek D;
 DR WPI; 1996-230552/23.
 XX
 XX Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 PT
 XX Example 9; Fig 1; 91pp; English.
 PS
 XX This sequence represents the human myelin oligodendrocyte protein (MOG).
 CC Immunisation with MOG (or the peptide fragments shown in
 CC AAR95375-R95385) can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for treating
 CC MS in a mammal. The composition acts to down regulate the autoimmune
 CC response, and may be administered in an amount sufficient to prevent the
 CC onset of symptoms of MS. The compositions may also be used to treat
 CC advanced stage MS, especially relapsing-remitting MS, chronic progressive
 CC MS or benign MS. These peptides may also be used in the treatment of
 CC other diseases involving myelin autoantigens, including diabetes, Graves
 CC disease, myasthenia gravis, Good Pasture's syndrome, psoriasis,
 CC thyroiditis, and rheumatoid arthritis. Peptides derived from other
 CC myelin autoantigens, such as myelin basic protein (MBP, see
 CC AAR95334-R95374), proteolipid protein (PLP), and myelin associated
 CC glycoprotein (MAG) can be used as alternatives to the MOG peptides in
 CC these compositions.
 XX
 XX Sequence 170 AA;
 SQ
 Query Match 100.0%; Score 103; DB 17; Length 170;
 Best Local Similarity 100.0%; Pred. No. 7.6e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGSLPQKSHGRTQDENP 18
 Db | | | | | | | | | | | | | | | | | |
 68 hygslpqkshgrtqdenp 85
 RESULT 5
 AAR97627
 ID AAR97627 standard; Protein; 171 AA.
 XX

AC AAR97627;
 XX 09-NOV-1996 (first entry)
 XX Human myelin basic protein.
 XX
 XX Myelin basic protein; MBP; multiple sclerosis; MS; treatment;
 KW prevention; analogue.
 KW
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Peptide 86..99
 FT /label= Claimed peptide region.
 XX
 XX W09616085-A1.
 PN
 XX 30-MAY-1996.
 PD
 XX 16-NOV-1995; 95WO-US14402.
 PF
 XX 18-NOV-1994; 94US-0342078.
 PR
 XX (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PA (STRD) UNIV STANFORD MEDICAL CENT.
 XX
 XX Conlon PJ, Gaur A, Ling N, Steinman L;
 PI WPI; 1996-268534/27.
 DR N-PSDB; AAT30269.
 XX
 XX Peptide analogue of human myelin basic protein - has Lysine 91
 PT replaced by another amino acid, useful to treat multiple sclerosis
 PT
 XX Claim 1; Figure 1; 30pp; English.
 PS
 XX A peptide analogue comprising amino acids 87-99 of human myelin
 CC basic protein (MBP), where lys91 is substituted for another amino
 CC acid can be used to treat and prevent multiple sclerosis. The
 CC peptide analogue is administered at a dosage range of 5-50 mg/kg.
 XX
 XX Sequence 171 AA;
 SQ
 Query Match 100.0%; Score 103; DB 17; Length 171;
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGSLPQKSHGRTQDENP 18
 Db | | | | | | | | | | | | | | | | | |
 69 hygslpqkshgrtqdenp 86
 RESULT 6
 AAR99580
 ID AAR99580 standard; Protein; 171 AA.
 XX
 XX AAR99580;
 AC
 XX 07-NOV-1996 (first entry)
 DT
 XX Human myelin basic protein (MBP).
 DE
 XX Myelin basic protein; MBP; multiple sclerosis; MS; competition;
 KW inhibition; major histocompatibility complex; MHC; thymocyte; T cell;
 KW experimental allergic encephalomyelitis; EAE; analogue.
 XX
 XX Homo sapiens.
 OS
 XX W09616086-A1.
 PN
 XX 30-MAY-1996.
 PD
 XX

| | | |
|-----------------|--|---------------|
| Pf | 16-NOV-1995; | 95WO-US14403. |
| Xx | | |
| Pr | 18-NOV-1994; | 94US-0342408. |
| Xx | | |
| Pa | (NEUR-) NEUROCRINE BIOSCIENCES INC. | |
| Xx | | |
| Pt | Conlon PJ, Gaur A, Ling N, Steinman L; | |
| Xx | | |
| Dd | WPI; 1996-268535/27. | |
| Dr | N-PSDB; AAT32561. | |
| Xx | | |
| Pt | Peptide analogues of human myelin basic protein - useful for treatment of multiple sclerosis | |
| Xx | | |
| Pt | Disclosure; Figure 1; 6lpp; English. | |
| Xx | | |
| Pt | Peptide analogues comprising at least seven amino acids from residues 86-99 of human myelin basic protein (MBP), can be used to treat multiple sclerosis by competing for the binding of native MBP peptide to MHC and by not causing proliferation of an MBP reactive T-cell line. The peptide analogues also inhibit the induction of experimental allergic encephalomyelitis (EAE) by MBP in rodents. | |
| Cc | The peptide analogues have a reduced susceptibility to proteolysis in vivo. | |
| Cc | Sequence 171 AA; | |
| Sq | | |
| Qy | Query Match 100.0%; Score 103; DB 17; Length 171; Best Local Similarity 100.0%; Pred. No. 7.7e-10; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Db | 1 HYGSLPKSHGRTQDENP 18 69 hygslpkshgtrqdnp 86 | |
| Rsult | 7 | |
| Aay27284 | | |
| ID | AAY27284 standard; Protein; 171 AA. | |
| XX | | |
| AC | AAY27284; | |
| XX | | |
| DT | 29-OCT-1999 (first entry) | |
| XX | | |
| DE | Human myelin basic protein (MBP). | |
| Kw | Myelin basic protein; MBP; peptide analogue; MHC; multiple sclerosis; T-cell reactivity; major histocompatibility complex; human. | |
| Kw | | |
| Kw | | |
| OS | Homo sapiens. | |
| XX | | |
| FH | Key Location/Qualifiers | |
| FT | Peptide 86..99 | |
| FT | /note= "peptide analogues of the invention comprise at least seven consecutive amino acid residues from this region" | |
| FT | | |
| Misc-difference | 97 | |
| FT | /note= "the L-Arg at this position can be altered to a D-amino acid and especially to a D-Ala to construct the peptide analogues (see claims 2 and 3" | |
| XX | | |
| PN | US5948764-A. | |
| XX | | |
| PD | 07-SEP-1999. | |
| XX | | |
| PF | 09-JAN-1997; 97US-0781122. | |
| XX | | |
| PR | 09-JAN-1997; 97US-0781122. | |
| PR | 09-MAR-1995; 95US-0402992. | |
| XX | | |
| XX | (NEUR-) NEUROCRINE BIOSCIENCES INC. | |

| | | |
|----------|---|--|
| XX | Conlon PJ, Gaur A, Ling N; | |
| PI | | |
| XX | WPI; 1999-517966/43. | |
| DR | N-PSDB; AA200399. | |
| XX | | |
| PT | Human myelin basic protein analogues useful for the treatment of multiple sclerosis | |
| XX | | |
| PS | Disclosure; Fig 1; 35pp; English. | |
| XX | | |
| CC | The invention provides human myelin basic protein (MBP) analogues. The analogues, comprise a sequence of 7 or more consecutive amino acids taken from between residues 86 to 99 of the native human MBP amino acid sequence (AAY27284). The analogues include residue 97 of the human MBP sequence, however, the L-arginine at position 97 is altered to a D-amino acid. The peptide analogues may be used for treating multiple sclerosis. Multiple sclerosis may be caused by an autoimmune reaction involving T-cells which have lost their 'self-tolerance' and attack normal tissue. Therefore, T-cell reactivity to human MBP may be a major cause of the development of MS. The T-cells recognize and bind to an epitope of human MBP between amino acids 86 to 106 of the sequence. The peptide analogues have a higher binding affinity for major histocompatibility complexes (MHC) on the T-cells than human MBP and therefore interfere with the reactivity of T-cells against human MBP. Administration of the analogues may prevent future, repeated attacks of multiple sclerosis without any side effects after long-term use (such as malignancies, toxic hepatitis and immunocompromising the patient). The present sequence represents a human MBP sequence. | |
| XX | | |
| SQ | Sequence 171 AA; | |
| QY | Query Match 100.0%; Score 103; DB 20; Length 171; Best Local Similarity 100.0%; Pred. No. 7.7e-10; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| DB | 1 HYGSLPKSHGRTQDENP 18 69 hygslpkshgtrqdnp 86 | |
| RESULT | 8 | |
| AAB19513 | | |
| ID | AAB19513 standard; Protein; 171 AA. | |
| XX | | |
| AC | AAB19513; | |
| XX | | |
| DT | 09-JAN-2001 (first entry) | |
| XX | | |
| DE | Human myelin basic protein. | |
| XX | | |
| KW | Myelin basic protein; human; autoimmune disease; autoantigen; demyelinating disease; experimental autoimmune encephalitis; multiple sclerosis; antiinflammatory; DNA vaccination; vaccine; T cell; pro-inflammatory response. | |
| KW | | |
| OS | Homo sapiens. | |
| XX | | |
| FN | WO200053019-A1. | |
| XX | | |
| PD | 14-SEP-2000. | |
| XX | | |
| PF | 10-MAR-2000; 2000MO-US06233. | |
| XX | | |
| PR | 12-MAR-1999; 99US-0267590. | |
| XX | | |
| PA | (STRD) UNIV LELAND STANFORD JUNIOR. | |
| XX | | |
| PI | Steinman L, Ruiz PJ, Garren H; | |
| XX | | |
| XX | WPI; 2000-587361/55. | |
| DR | N-PSDB; AAA50667. | |

XX Treating an autoimmune disease in a mammalian host by introducing a DNA
 PT expression cassette comprising a sequence encoding a portion of an
 PT autoantigen associated with a pro-inflammatory Th1-type T cell response
 PT -
 XX
 PS Disclosure: Page 42; 50pp; English.
 XX
 CC The present sequence is that of human myelin basic protein. The
 CC invention provides methods for the suppression of pro-inflammatory
 CC T cell responses in autoimmune disease. A mammalian host is
 CC vaccinated with a DNA expression vector encoding an autoantigen
 CC fragment, e.g. from myelin basic protein. In response to the
 CC vaccination, pathogenic T cell proliferation is inhibited and
 CC production of Th1 cytokines, including interleukin-2,
 CC interferon-gamma and interleukin-15, is reduced. Suppressive
 CC vaccination diminishes T cell pro-inflammatory responses in a
 CC specific, targeted manner. Conditions that benefit from this
 CC treatment include autoimmune diseases, tissue transplantation and
 CC other conditions associated with inflammation. Autoimmune
 CC diseases that can be treated include demyelinating diseases such as
 CC experimental autoimmune encephalitis and multiple sclerosis
 CC (claimed).
 XX

SQ Sequence 171 AA;

Query Match 100.0%; Score 103; DB 21; Length 171;
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGSLPQKSHGRTQDENP 18
 | | | | | | | | | | | | | | | | | | | | | |
 Db 69 hygslpqkshgtrtdenp 86

RESULT 9

AAAY69394

ID AAY69394 standard; Protein; 171 AA.

XX AAY69394;

AC AAY69394;

XX 19-JUN-2000 (first entry)

XX Amino acid sequence of a human myelin basic protein.

XX Human; myelin basic protein; oligodendroglial cell; Th2 immune response;
 KW Th2-type cytokine; analogue; multiple sclerosis.
 XX

OS Homo sapiens.

XX WO200011027-A1.

XX 02-MAR-2000.

XX 19-AUG-1999; 99WO-US19033.

XX 20-AUG-1998; 98US-0137759.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PA (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;

XX WPI; 2000-224661/19.

DR N-PSDB; AA261594.

XX Inducing a Th2 immune response and a persistent systemic immune
 PT response to myelin basic protein, MBP, or a peptide analog of MBP for
 PT use in treating multiple sclerosis, by administering compositions
 PT comprising peptide analogs of MBP
 XX

PS Disclosure: Fig 1; 112pp; English.

XX The present sequence represents a human myelin basic protein. Myelin
 CC basic protein is found in the cytoplasm of human oligodendroglial
 CC cells. Peptide analogues of myelin basic protein are administered to
 CC a patient in need to induce a Th2 immune response (i.e. production
 CC of T cells producing one or more Th2-type cytokines) and/or a
 CC persistent systemic immune response to myelin basic protein. These
 CC peptide analogues are at least seven amino acids long, derived from
 CC residues 83-99 of human myelin basic protein and altered from the
 CC native sequence at least at positions 91, 95 or 97. The peptide
 CC analogs are especially useful in the treatment of multiple sclerosis.

XX Sequence 171 AA;

Query Match 100.0%; Score 103; DB 21; Length 171;
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGSLPQKSHGRTQDENP 18
 | | | | | | | | | | | | | | | | | | | | | |
 Db 69 hygslpqkshgtrtdenp 86

RESULT 10

AAAY44234

ID AAY44234 standard; Protein; 171 AA.

XX AAY44234;

AC AAY44234;

XX 21-FEB-2000 (first entry)

XX Human myelin basic protein.

XX Human; myelin basic protein; MBP; NS-specific antigen;
 KW nervous system-specific antigen; T cell; peripheral nervous system; PNS;
 KW central nervous system; CNS; nerve regeneration; neuronal degeneration;
 KW spinal cord injury; blunt trauma; penetrating trauma; senile dementia;
 KW ischaemic stroke; diabetic neuropathy; glaucoma; haemorrhagic stroke;
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
 KW amyotrophic lateral sclerosis; ALS; treatment.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT 11..30

FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"

FT Peptide 51..70

FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"

FT Peptide 91..110

FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"

FT Peptide 131..150

FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"

FT Peptide 151..170

FT /label= Cryptic epitope
 FT /note= "activates T cells by itself but does not
 FT induce an autoimmune disease"

XX WO9960021-A2.

XX 25-NOV-1999.

XX 19-MAY-1999; 99WO-US10953.

PR 19-MAY-1998; 98IL-0124550.
 PR 21-JUL-1998; 98WO-US14715.
 XX 22-DEC-1998; 98US-0218277.
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA (MCIN) MCINNIS P A.
 XX Eisenbach-Schwartz M, Cohen IR, Beserman P, Mosonogo A, Moalem G;
 DR WPI; 2000-072430/06.
 DR N-PSDB; AA229197.
 XX New compositions useful to treat nervous system injury or disease e.g.
 PT traumatic injury, Alzheimer's disease etc.
 PT Claim 9; Fig 21; 92pp; English.
 XX The present sequence is a human myelin basic protein
 CC which is a nervous system-specific antigen. The antigen or peptides
 CC derived from it activate T cells in vivo. The present sequence is
 CC used to promote nerve regeneration or to prevent or inhibit neuronal
 CC degeneration caused by injury or diseases of nerves within the CNS or
 CC PNS. Such injury includes spinal cord injury, blunt trauma, penetrating
 CC trauma, haemorrhagic stroke or ischaemic stroke, whilst diseases include
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis,
 CC etc.
 XX Sequence 171 AA;

Query Match 100.0%; Score 103; DB 21; Length 171;
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 |||||
 Db 69 hygslpqkshgtrtdenp 86

RESULT 11

AA57090
 ID AAY57090 standard; protein; 186 AA.

AC AAY57090;

DT 28-FEB-2000 (first entry)

DE Human myelin basic protein fragment.

XX Neglected target tissue antigen; NNTA; autoimmunity; autoimmune response;
 KW immunotherapeutic agent; insulin dependent diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
 KW uveoretinitis; inflammatory response.

XX Homo sapiens.

XX WO956763-A1.

XX 11-NOV-1999.

XX 07-MAY-1999; 99WO-US10250.

XX 07-MAY-1998; 98US-0084636.

XX (REGC) UNIV CALIFORNIA.

XX Kaufman DL, Tian J, Olcott A;

XX WPI; 2000-052905/04.

XX Administration of neglected target tissue antigens to modulate immune
 PT responses

XX Disclosure; Page 33; 79pp; English.
 XX Amino acid sequences AAY57063-Y57091 are examples of neglected target
 CC tissue antigens NNTAs. NNTAs are antigens (whole antigens or fragments)
 CC not involved in autoimmunity. These peptides and proteins are used in
 CC the method of the invention which involves administering an NNTA as an
 CC antigen based immunotherapeutic agent, to a host afflicted with an
 CC autoimmune response associated with an autoimmune disease. The
 CC immunotherapeutic agent is used to treat autoimmune diseases such as
 CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
 CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal
 CC inflammatory immune responses. The NNTA induces regulatory tolerance by
 CC elicitation of regulatory T cells among T cells recognizing the NNTA but
 CC not participating in the immune response. The NNTA are capable of
 CC recognition by substantial populations of uncommitted T cells which can
 CC be primed, or biased, towards regulatory responses to provide effective
 CC treatment. The NNTA are effective in regulating undesirable immune
 CC responses even when target determinants used as agents promoting
 CC tolerance agents have failed to induce an effective regulatory T cell
 CC response. NNTAs as agents promoting tolerance are anticipated to be safer
 CC than use of target determinants.
 XX Sequence 186 AA;

Query Match 100.0%; Score 103; DB 21; Length 186;
 Best Local Similarity 100.0%; Pred. No. 8.4e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 |||||
 Db 95 hygslpqkshgtrtdenp 112

RESULT 12

AAW00399

ID AAW00399 standard; Protein; 197 AA.

AC AAW00399;

DT 01-FEB-1997 (first entry)

DE Human myelin basic protein (foetal isoform).

XX Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KW T-lymphocyte; T-cell; anergy; apoptosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 60..85

FT /label= X2

FT Misc-difference 81 /note= "exon 2-encoded region"

FT /note= "Cys-81 may be replaced by any standard
 FT amino acid, esp. an uncharged amino acid
 FT of mol.wt. below about 150, partic.
 FT Ser, in constructs of the invention"

XX WO9634622-A1.

XX 07-NOV-1996.

XX 22-APR-1996; 96WO-US05611.

XX 07-JUN-1995; 95US-0482114.

XX 02-MAY-1995; 95US-0431644.

XX 02-MAY-1995; 95US-0431648.

XX (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI: 1996-505898/50.
 DR N-PSDB; AAT41889.
 XX New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 CC
 PS Claim 1; Page 79-80; 156pp; English.
 XX The native human 21.5 kDa foetal isoform (AAW00399) of myelin basic
 CC protein, MBP+X2Cys81, includes an exon 2-encoded region (X2) that
 CC may contain an epitope involved in the pathogenesis of multiple
 CC sclerosis (MS); the X2 region is not found in the MBP of healthy
 CC adults. Recombinant MBP+X2, or variants modified to improve
 CC bacterial expression (see also AAW06107), can be produced in a
 CC large scale in bacterial hosts. They are useful for assaying
 CC T-cells for responsiveness to MBP epitopes and can be used as
 CC therapeutic agents that act by inducing T-cell responses,
 CC including energy and apoptosis, as a means of treating MS.
 XX
 XX Sequence 197 AA;
 SQ

Query Match 100.0%; Score 103; DB 17; Length 197;
 Best Local Similarity 100.0%; Pred. No. 9e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 Db 95 hygsipqkshgtrtdenp 112
 |||||

RESULT 13
 ID AAY95922 standard; Protein; 197 AA.
 XX
 AC AAY95922;
 XX
 DT 20-NOV-2000 (first entry)
 XX
 DE Human myelin binding protein Delta II.
 XX
 KW goodpasture antigen binding protein; autoimmune disease; apoptosis;
 KW cancer; tumour; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2000050607-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 24-FEB-2000; 2000WO-IB00324.
 XX
 PR 24-FEB-1999; 99US-0121483.
 XX
 PA (SAUS/) SAUS J.
 XX
 PI Saus J;
 XX
 DR WPI: 2000-572094/53.
 DR N-PSDB; AAW50371.
 XX
 XX Novel Goodpasture antigen binding proteins useful for diagnosing and
 PT treating autoimmune disorders, tumor, and preventing cell apoptosis -
 XX
 PS Claim 36; Page 157; 158pp; English.
 XX
 CC The present sequence is that of human myelin binding protein (MBP)

CC Delta II, i.e. an alternative form of human MBP resulting from
 CC splicing out of exon II. The protein was recombinantly expressed in
 CC Pichia pastoris cells. The invention relates to novel Goodpasture
 CC antigen binding proteins (GPBPs, see AAY95900-11), which bind to and
 CC phosphorylate the unique N-terminal region of human GP, and which
 CC are highly expressed in several autoimmune conditions. Claimed
 CC methods for treating an autoimmune disorder, cell apoptosis or a
 CC tumour involve modifying the expression or activity of GPBP,
 CC especially using a MBP protein or a nucleic acid sequence encoding
 CC it.
 XX
 XX Sequence 197 AA;
 SQ

Query Match 100.0%; Score 103; DB 21; Length 197;
 Best Local Similarity 100.0%; Pred. No. 9e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 Db 95 hygsipqkshgtrtdenp 112
 |||||

RESULT 14
 ID AAW06107 standard; Protein; 203 AA.
 XX
 AC AAW06107;
 XX
 DT 01-FEB-1997 (first entry)
 XX
 DE Foetal myelin basic protein MBP+X2Cys81/bact.
 XX
 KW Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KW T-lymphocyte; T-cell; anergy; apoptosis.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Region 60..85
 FT /label= X2
 FT /note= "exon 2-encoded region"
 XX
 PN WO9634622-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 22-APR-1996; 96WO-US05611.
 XX
 PR 07-JUN-1995; 95US-0482114.
 PR 02-MAY-1995; 95US-0431644.
 PR 02-MAY-1995; 95US-0431648.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 XX
 DR WPI: 1996-505898/50.
 DR N-PSDB; AAT41896.
 XX
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 XX
 PS Disclosure; Page 81-82; 156pp; English.
 CC A 21.5 kDa foetal isoform (AAW06107) of myelin basic protein,
 CC MBP+X2Cys81/bact., is the product of a DNA construct (AAT41896)
 CC based on the human foetal MBP+X2Cys81 isoform (AAW00399) but
 CC utilising bacterially-preferred codons in place of the native human

CC codons (see also AAT41889). This increases prodn. of the MBP in E.
 CC coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also
 CC AAW00399 and AAW06108) are useful in the clinical assessment, diagnosis
 CC and treatment of MS.

XX Sequence 203 AA;

Query Match 100.0%; Score 103; DB 17; Length 203;
 Best Local Similarity 100.0%; Pred. No. 9.3e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 |||||
 Db 95 hygslpqkshgrtgdenp 112

RESULT 15

AAW06108
 ID AAW06108 standard; Protein; 203 AA.

XX AC AAW06108;

XX DT 01-FEB-1997 (first entry)

XX DE Foetal myelin basic protein MBP+X2Ser81/bact.

XX KW Myelin basic protein; MBP; MBP+X2Ser81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 XX T-lymphocyte; T-cell; anergy; apoptosis.

OS Synthetic.

XX FH Key Location/Qualifiers
 FT Region 60..85
 FT /label= X2
 FT /note= "exon 2-encoded region, with Cys81Ser
 FT mutation"

FT Peptide

FT 198..203

FT /label= "Hexa-histidine tag
 FT /note= "the hexa-histidine tag facilitates
 FT purification of the recombinant protein
 FT from host cells"

XX PN W09634622-A1.

XX PD 07-NOV-1996.

XX PF 22-APR-1996; 96WO-US05611.

XX PR 07-JUN-1995; 95US-0482114.

XX PR 02-MAY-1995; 95US-0431644.

XX PR 02-MAY-1995; 95US-0431648.

XX PA (ALEX-) ALEXION PHARM INC.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;

XX DR WPI; 1996-505898/50.

XX DR N-PSDB; AAT41897.

XX PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis

XX PS Disclosure; Page 82-83; 156pp; English.

XX CC A 21.5 kDa foetal isoform (AAW06108) of myelin basic protein.
 CC MBP+X2Ser81/bact., is the product of a DNA construct (AAT41897)
 CC based on the human foetal MBP+X2Cys81 isoform (AAW00399) but
 CC utilising codons that are highly expressed in bacterial genes in

CC place of the native codons (see also AAT41889) and incorporating a
 CC sequence coding for a hexa-histidine tail. This allows large-
 CC scale prodn. and purification of the MBP in bacterial hosts.
 CC Recombinant MBP 21.5 polypeptides (see also AAW00399 and AAW06107) are
 CC useful in the clinical assessment, diagnosis and treatment of MS.

XX Sequence 203 AA;

Query Match 100.0%; Score 103; DB 17; Length 203;
 Best Local Similarity 100.0%; Pred. No. 9.3e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 |||||
 Db 95 hygslpqkshgrtgdenp 112

Search completed: August 28, 2002, 16:35:03
 Job time: 285 sec

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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:35:30 ; Search time 20.54 Seconds
(without alignments)
21.405 Million cell updates/sec

Title: US-09-813-383-1_COPY_8_25

Perfect score: 103

Sequence: 1 HYGSLPQKSHGRTQDENP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|-------------------|
| 1 | 103 | 100.0 | 170 | 2 | US-08-327-357A-1 |
| 2 | 103 | 100.0 | 170 | 3 | US-09-007-520-1 |
| 3 | 103 | 100.0 | 170 | 4 | US-09-056-263-1 |
| 4 | 103 | 100.0 | 170 | 4 | US-09-007-520-1 |
| 5 | 103 | 100.0 | 170 | 4 | US-08-342-408B-2 |
| 6 | 103 | 100.0 | 171 | 2 | US-08-781-122-2 |
| 7 | 103 | 100.0 | 171 | 4 | US-09-137-759-2 |
| 8 | 85 | 82.5 | 168 | 6 | 5194425-4 |
| 9 | 82 | 79.6 | 20 | 3 | US-08-297-395-21 |
| 10 | 82 | 79.6 | 40 | 3 | US-08-297-395-2 |
| 11 | 75.5 | 73.3 | 170 | 1 | US-08-227-372-1 |
| 12 | 75.5 | 73.3 | 170 | 3 | US-08-462-361-3 |
| 13 | 75.5 | 73.3 | 170 | 6 | 5194425-3 |
| 14 | 75.5 | 73.3 | 170 | 6 | 5468481-3 |
| 15 | 74.5 | 72.3 | 170 | 3 | US-08-470-397-1 |
| 16 | 74 | 71.8 | 20 | 2 | US-08-468-540B-8 |
| 17 | 74 | 71.8 | 20 | 3 | US-08-297-395-20 |
| 18 | 67 | 65.0 | 20 | 1 | US-08-787-547-35 |
| 19 | 66.5 | 64.6 | 17 | 4 | US-09-123-485-1 |
| 20 | 66 | 64.1 | 20 | 2 | US-08-468-540B-7 |
| 21 | 63.5 | 61.7 | 19 | 4 | US-09-153-586-30 |
| 22 | 59.5 | 57.8 | 19 | 4 | US-09-153-586-25 |
| 23 | 58.5 | 56.8 | 13 | 2 | US-08-596-387B-9 |
| 24 | 58.5 | 56.8 | 13 | 4 | US-09-067-615-9 |
| 25 | 58.5 | 56.8 | 13 | 5 | PCT-US95-09816A-9 |
| 26 | 54.5 | 52.9 | 15 | 2 | US-08-735-253-18 |
| 27 | 53.5 | 51.9 | 18 | 2 | US-08-468-540B-14 |

| | | | | | | |
|----|------|------|------|---|---------------------|-------------------|
| 28 | 49.5 | 48.1 | 37 | 4 | US-09-153-586-4 | Sequence 4, Appli |
| 29 | 48 | 46.6 | 9 | 3 | US-08-159-339A-1079 | Sequence 1079, Ap |
| 30 | 46 | 44.7 | 10 | 3 | US-08-159-339A-1096 | Sequence 1096, Ap |
| 31 | 45 | 43.7 | 23 | 1 | US-08-787-547-1 | Sequence 1, Appli |
| 32 | 45 | 43.7 | 24 | 1 | US-08-305-871A-2 | Sequence 2, Appli |
| 33 | 45 | 43.7 | 24 | 2 | US-08-480-190-46 | Sequence 46, Appl |
| 34 | 45 | 43.7 | 24 | 2 | US-08-488-379-46 | Sequence 46, Appl |
| 35 | 45 | 43.7 | 24 | 5 | PCT-US93-07545-46 | Sequence 46, Appl |
| 36 | 44 | 42.7 | 1312 | 4 | US-09-041-886-19 | Sequence 19, Appl |
| 37 | 42 | 40.8 | 1865 | 4 | US-08-588-985-2 | Sequence 2, Appli |
| 38 | 42 | 40.8 | 1865 | 1 | US-08-971-988-2 | Sequence 2, Appli |
| 39 | 41.5 | 40.3 | 475 | 2 | US-08-819-825-2 | Sequence 2, Appli |
| 40 | 41.5 | 40.3 | 475 | 4 | US-09-163-642-2 | Sequence 19, Appl |
| 41 | 41 | 39.8 | 107 | 4 | US-08-098-327E-19 | Sequence 19, Appl |
| 42 | 41 | 39.8 | 107 | 4 | US-08-462-625-19 | Sequence 19, Appl |
| 43 | 41 | 39.8 | 117 | 4 | US-08-098-327E-20 | Sequence 20, Appl |
| 44 | 41 | 39.8 | 117 | 4 | US-08-462-625-20 | Sequence 20, Appl |
| 45 | 41 | 39.8 | 316 | 4 | US-08-098-327E-31 | Sequence 31, Appl |

ALIGNMENTS

RESULT 1
US-08-327-357A-1
; Sequence 1, Application US/08327357A
; Patent No. 5817629

; GENERAL INFORMATION:

; APPLICANT: WARREN, Kenneth G.

; APPLICANT: CATZ, Ingrid

; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC

; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN

; TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard & Civiletti

; STREET: 1201 New York Avenue, N.W., Suite 1000

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/327,357A

; FILING DATE: 21-OCT-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/798,099

; FILING DATE: 27-NOV-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: CA 2,053,799-0

; FILING DATE: 22-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Ihnen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 27052-115469

; TELEPHONE: 202-962-4810

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; IMMEDIATE SOURCE:

CLONE: human myelin basic protein
US-08-327-357A-1

Query Match 100.0%; Score 103; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 2

US-09-007-520-1
; Sequence 1, Application US/09007520
; Patent No. 6103696
; GENERAL INFORMATION:
; APPLICANT: WARREN, Kenneth G.
; APPLICANT: CATZ, Ingrid
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
; TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007.520
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327.357
; FILING DATE:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 27052-115469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: human myelin basic protein
US-09-007-520-1

Query Match 100.0%; Score 103; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 3

US-09-055-263-1
; Sequence 1, Application US/09055263
; Patent No. 6252040
; GENERAL INFORMATION:
; APPLICANT: WARREN, Kenneth G.
; APPLICANT: CATZ, Ingrid
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
; TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
; TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055.263
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/327.357
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: US 07/798,099
; FILING DATE: 27-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 27052-115469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: human myelin basic protein
US-09-055-263-1

Query Match 100.0%; Score 103; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
|||||

Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 4

US-09-007-520-1
; Sequence 1, Application US/09007520
; Patent No. 6258781
; GENERAL INFORMATION:

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; APPLICANT: WARREN, Kenneth G.
; CATZ, Ingrid
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
; PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
; PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
;
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/007,520
; APPLICATION NUMBER: 08/327,357
; FILING DATE: 15-Jan-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/327,357
; FILING DATE: <Unknown>
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 27052-115469
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: human myelin basic protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-007-520-1

Query Match 100.0%; Score 103; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18
Db 68 HYGSLPKSHGRTQDENP 85

RESULT 5
US-08-342-408B-2
; Sequence 2, Application US/08342408B
; Patent No. 6329499
; GENERAL INFORMATION:
; APPLICANT: Ling, Nicholas
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Steinman, Lawrence
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
; SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC
; PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,122
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

```

```

; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,408B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6329499tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 690068.405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-342-408B-2

Query Match 100.0%; Score 103; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18
Db 68 HYGSLPKSHGRTQDENP 85

RESULT 6
US-08-781-122-2
; Sequence 2, Application US/08781122
; Patent No. 5948764
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS
; UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,122
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

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; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 171 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-781-122-2

Query Match 100.0%; Score 103; DB 2; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3.7e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 Db 69 HYGSLPQKSHGRTQDENP 86

RESULT 7
 US-09-137-759-2
 ; Sequence 2, Application US/09137759
 ; Patent No. 6251396
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaur, Amitabh
 ; APPLICANT: Conlon, Paul J.
 ; APPLICANT: Ling, Nicholas C.
 ; APPLICANT: Staehlin, Theophil
 ; APPLICANT: Crowe, Paul D.
 ; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
 ; FILE REFERENCE: 630068.405C1
 ; CURRENT APPLICATION NUMBER: US/09/137,759
 ; CURRENT FILING DATE: 1998-08-20
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 171
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-137-759-2

Query Match 100.0%; Score 103; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 3.7e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 Db 69 HYGSLPQKSHGRTQDENP 86

RESULT 8
 5194425-4
 ; Patent No. 5194425
 ; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
 ; BRIAN R.
 ; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
 ; AMELIORATING AUTOIMMUNITY
 ; NUMBER OF SEQUENCES: 9
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/367,751
 ; FILING DATE: 21-JUN-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 210,594
 ; FILING DATE: 23-JUN-1988
 ; SEQ ID NO: 4
 ; LENGTH: 168
 ; 5194425-4

Query Match 82.5%; Score 85; DB 6; Length 168;
 Best Local Similarity 88.9%; Pred. No. 4.1e-07;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 Db 66 HYGSLPQKSHGRTQDENP 83

RESULT 9
 US-08-297-395-21
 ; Sequence 21, Application US/08297395A
 ; Patent No. 6039947
 ; GENERAL INFORMATION:
 ; APPLICANT: Howard L. Weiner
 ; APPLICANT: David A. Hafler
 ; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
 ; FILE REFERENCE: 1010/05723US3
 ; CURRENT APPLICATION NUMBER: US/08/297,395A
 ; CURRENT FILING DATE: 1994-08-11
 ; EARLIER APPLICATION NUMBER: 08/059,189
 ; EARLIER FILING DATE: 1993-05-06
 ; EARLIER APPLICATION NUMBER: 07/502,559
 ; EARLIER FILING DATE: 1990-03-30
 ; EARLIER APPLICATION NUMBER: PCT/US88/02139
 ; EARLIER FILING DATE: 1988-06-24
 ; EARLIER APPLICATION NUMBER: 07/065,734
 ; EARLIER FILING DATE: 1987-06-24
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-297-395-21

Query Match 79.6%; Score 82; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SLPQKSHGRTQDENP 18
 Db 1 SLPQKSHGRTQDENP 15

RESULT 10
 US-08-297-395-2
 ; Sequence 2, Application US/08297395A
 ; Patent No. 6039947
 ; GENERAL INFORMATION:
 ; APPLICANT: Howard L. Weiner
 ; APPLICANT: David A. Hafler
 ; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
 ; FILE REFERENCE: 1010/05723US3
 ; CURRENT APPLICATION NUMBER: US/08/297,395A
 ; CURRENT FILING DATE: 1994-08-11
 ; EARLIER APPLICATION NUMBER: 08/059,189
 ; EARLIER FILING DATE: 1993-05-06
 ; EARLIER APPLICATION NUMBER: 07/502,559
 ; EARLIER FILING DATE: 1990-03-30
 ; EARLIER APPLICATION NUMBER: PCT/US88/02139
 ; EARLIER FILING DATE: 1988-06-24
 ; EARLIER APPLICATION NUMBER: 07/065,734
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 40
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-297-395-2

Query Match 79.6%; Score 82; DB 3; Length 40;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SLPOKSHGRTDQNP 18
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 DB 1 SLPOKSHGRTDQNP 15

RESULT 11
 US-08-227-372-1
 ; Sequence 1, Application US/08227372
 ; Patent No. 5763585
 ; GENERAL INFORMATION:
 ; APPLICANT: Nag, Bishwajit
 ; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
 ; MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourlie and Crew
 ; STREET: Stewart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94105-1493
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/227,372
 ; FILING DATE: 14-APR-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/136,216
 ; FILING DATE: 13-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bastian, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 14058-32-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 170 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..170
 ; OTHER INFORMATION: /note= "Myelin basic protein"
 ; US-08-227-372-1

Query Match 73.3%; Score 75.5; DB 1; Length 170;
 Best Local Similarity 78.9%; Pred. No. 1.7e-05;
 Matches 15; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 HYGSLPQKSHG-RTQDQNP 18
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 DB 67 HYGSLPQKSHGRTDQNP 85

RESULT 12
 US-08-462-351-3
 ; Sequence 3, Application US/08462351
 ; Patent No. 6106840
 ; GENERAL INFORMATION:
 ; APPLICANT: Sharma, Somesh D.
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME/KEY: Clark, Brian R.

APPLICANT: Lerch, Bernard L.
 TITLE OF INVENTION: MHC Conjugates Useful in Ameliorating
 ; TITLE OF INVENTION: Autoimmunity
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,351
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/210,594
 ; FILING DATE: 23-JUN-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/576,084
 ; FILING DATE: 30-AUG-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/690,840
 ; FILING DATE: 23-APR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/869,293
 ; FILING DATE: 14-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parent, Annette S.
 ; REGISTRATION NUMBER: 42,058
 ; REFERENCE/DOCKET NUMBER: 014058-000242US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 170 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..170
 ; OTHER INFORMATION: /note= "myelin basic protein (MBP)"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /product= "OTHER"
 ; OTHER INFORMATION: /note= "Xaa = N-acetyl-alanine"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 3
 ; OTHER INFORMATION: /product= "OTHER"
 ; OTHER INFORMATION: /note= "Ala at position 3 may be present
 ; OTHER INFORMATION: or absent"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 10
 ; OTHER INFORMATION: /product= "OTHER"
 ; OTHER INFORMATION: /note= "Xaa = Arg or His"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 11
 ; OTHER INFORMATION: /product= "OTHER"
 ; OTHER INFORMATION: /note= "Xaa = Ser or Gly"
 ; FEATURE:
 ; NAME/KEY: Modified-site

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; LOCATION: 16
; OTHER INFORMATION: /product= "OTHER"
; FEATURE:
; OTHER INFORMATION: /note= "Xaa = Ser or Thr"
; NAME/KEY: Modified-site
; LOCATION: 40
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = Leu or Ile"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 46
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = Ser or Gly"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 59
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = Gly or Ser"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 66
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = Thr or Ala"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 75
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = Ala or Ser"
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; NAME/KEY: Modified-site
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; OTHER INFORMATION: /note= "Gln at position 76 may be
; OTHER INFORMATION: present or absent"
; FEATURE:
; NAME/KEY: Modified-site
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; OTHER INFORMATION: /note= "Xaa = Pro or Thr"
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; NAME/KEY: Modified-site
; LOCATION: 107
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = Arg or Met"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 122
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = Lys or Arg"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 141
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = Leu or Phe"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 144
; OTHER INFORMATION: /product= "OTHER"
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; US-08-462-351-3

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Query Match 73.3%; Score 75.5; DB 3; Length 170;
Best Local Similarity 78.9%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 HYGSLPQKSHG-RTODENP 18
Db 67 HYGSLPQKXGHRXQDENP 85

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RESULT 13
5194425-3

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; Patent No. 5194425
; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
; BRIAN R.
; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
; AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION NUMBER: US/07/367,751
; FILING DATE: 21-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; SEQ ID NO: 3:
; LENGTH: 170
; 5194425-3

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Query Match 73.3%; Score 75.5; DB 6; Length 170;
Best Local Similarity 78.9%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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Qy 1 HYGSLPQKSHG-RTODENP 18
Db 67 HYGSLPQKXGHRXQDENP 85

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RESULT 14
5468481-3
; Patent No. 5468481
; APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L.
; TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL
; IN AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,293
; FILING DATE: 14-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 690,840
; FILING DATE: 23-APR-1991
; APPLICATION NUMBER: 576,084
; FILING DATE: 30-AUG-1990
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; APPLICATION NUMBER: 635,840
; FILING DATE: 28-DEC-1996
; APPLICATION NUMBER: 367,751
; FILING DATE: 21-JUN-1989
; SEQ ID NO: 3:
; LENGTH: 170
; 5468481-3

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Query Match 73.3%; Score 75.5; DB 6; Length 170;
Best Local Similarity 78.9%; Pred. No. 1.7e-05;
Matches 15; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy 1 HYGSLPQKSHG-RTODENP 18
Db 67 HYGSLPQKXGHRXQDENP 85

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RESULT 15
US-08-470-397-1
; Sequence 1, Application US/08470397
; Patent No. 6007820
; GENERAL INFORMATION:
; APPLICANT: Nag, Bishwajit
; TITLE OF INVENTION: Purification and Characterization of
; MHC-Peptide Complexes Useful in Ameliorating Autoimmunity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower, 20th

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; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,397
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136,216
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,372
; FILING DATE: 14-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14058-32-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
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; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = N-acetyl-alanine"
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; NAME/KEY: Modified-site
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; NAME/KEY: Modified-site
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; FEATURE:
; NAME/KEY: Modified-site
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; NAME/KEY: Modified-site
; LOCATION: 66
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 80
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; OTHER INFORMATION: /note= "Xaa = Pro or Thr"
; FEATURE:
; NAME/KEY: Modified-site
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; OTHER INFORMATION: /product= "OTHER"
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 144
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = His or Val"
; FEATURE:
; NAME/KEY: Protein
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; US-08-470-397-1
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; Query Match 72.3%; Score 74.5; DB 3; Length 170;
; Best Local Similarity 78.9%; Pred. No. 2.5e-05;
; Matches 15; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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; QY 1 HYGSLPQKSHG-RTQDENP 18
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; DB 67 HYGSLPQKSHG-RTQDENP 85
;
; Search completed: August 28, 2002, 16:35:30
; Job time: 192 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:39:34 ; Search time 205.27 Seconds
(without alignments)
30.865 Million cell updates/sec

Title: US-09-813-383-1_COPY_8_25
Perfect score: 103
Sequence: 1 HYGSLPQKSHGRTQDENP 18

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Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query # | | | Description | |
|------------|---------|-------|--------|-------------|--------------------|
| | Score | Match | Length | DB | ID |
| 1 | 103 | 100.0 | 46 | 22 | US-09-813-383-1 |
| 2 | 103 | 100.0 | 108 | 21 | US-09-760-443-1465 |
| 3 | 103 | 100.0 | 108 | 21 | US-09-760-495-898 |
| 4 | 103 | 100.0 | 136 | 21 | US-09-760-443-1435 |
| 5 | 103 | 100.0 | 136 | 21 | US-09-760-495-651 |
| 6 | 103 | 100.0 | 167 | 3 | US-07-987-751-3 |
| 7 | 103 | 100.0 | 168 | 3 | US-07-987-751-4 |
| | | | | | Sequence 1, Appli |
| | | | | | Sequence 1465, Ap |
| | | | | | Sequence 898, App |
| | | | | | Sequence 1435, App |
| | | | | | Sequence 651, App |
| | | | | | Sequence 3, Appli |
| | | | | | Sequence 4, Appli |

| | | | | | | |
|----|------|-------|-----|----|----------------------|--------------------|
| 8 | 103 | 100.0 | 170 | 3 | US-07-798-099A-1 | Sequence 1, Appli |
| 9 | 103 | 100.0 | 170 | 6 | US-08-241-246-1 | Sequence 1, Appli |
| 10 | 103 | 100.0 | 170 | 6 | US-08-241-246B-1 | Sequence 1, Appli |
| 11 | 103 | 100.0 | 170 | 7 | US-08-327-357-1 | Sequence 1, Appli |
| 12 | 103 | 100.0 | 170 | 7 | US-08-328-224-5 | Sequence 5, Appli |
| 13 | 103 | 100.0 | 170 | 8 | US-08-342-078-2 | Sequence 2, Appli |
| 14 | 103 | 100.0 | 170 | 8 | US-08-404-228-1 | Sequence 1, Appli |
| 15 | 103 | 100.0 | 170 | 8 | US-08-462-941A-1 | Sequence 1, Appli |
| 16 | 103 | 100.0 | 170 | 8 | US-08-463-412-1 | Sequence 1, Appli |
| 17 | 103 | 100.0 | 170 | 8 | US-08-463-456-1 | Sequence 1, Appli |
| 18 | 103 | 100.0 | 170 | 8 | US-08-481-938-1 | Sequence 1, Appli |
| 19 | 103 | 100.0 | 170 | 24 | US-10-015-340-2 | Sequence 2, Appli |
| 20 | 103 | 100.0 | 171 | 1 | PCT-US00-06233-1 | Sequence 4, Appli |
| 21 | 103 | 100.0 | 171 | 7 | US-08-342-078A-2 | Sequence 2, Appli |
| 22 | 103 | 100.0 | 171 | 8 | US-08-484-409-2 | Sequence 2, Appli |
| 23 | 103 | 100.0 | 171 | 13 | US-08-953-937-2 | Sequence 12, Appli |
| 24 | 103 | 100.0 | 171 | 16 | US-09-218-277-12 | Sequence 4, Appli |
| 25 | 103 | 100.0 | 171 | 16 | US-09-267-590-4 | Sequence 12, Appli |
| 26 | 103 | 100.0 | 171 | 17 | US-09-314-161-12 | Sequence 2, Appli |
| 27 | 103 | 100.0 | 171 | 17 | US-09-378-244-2 | Sequence 12, Appli |
| 28 | 103 | 100.0 | 171 | 22 | US-09-893-348-12 | Sequence 4, Appli |
| 29 | 103 | 100.0 | 171 | 23 | US-09-947-770-4 | Sequence 2, Appli |
| 30 | 103 | 100.0 | 171 | 23 | US-09-989-476-2 | Sequence 12, Appli |
| 31 | 103 | 100.0 | 171 | 24 | US-10-000-439-12 | Sequence 12, Appli |
| 32 | 103 | 100.0 | 176 | 1 | PCT-US01-14627-13007 | Sequence 13007, A |
| 33 | 103 | 100.0 | 183 | 1 | PCT-US01-08656-9330 | Sequence 9330, Ap |
| 34 | 103 | 100.0 | 186 | 17 | US-09-310-707A-28 | Sequence 28, Appl |
| 35 | 103 | 100.0 | 197 | 19 | US-09-512-563-54 | Sequence 54, Appl |
| 36 | 103 | 100.0 | 197 | 19 | US-09-512-563A-54 | Sequence 54, Appl |
| 37 | 103 | 100.0 | 197 | 19 | US-09-512-563C-54 | Sequence 54, Appl |
| 38 | 103 | 100.0 | 203 | 18 | US-09-463-186-1 | Sequence 1, Appli |
| 39 | 103 | 100.0 | 305 | 21 | US-09-760-443-1502 | Sequence 1502, Ap |
| 40 | 103 | 100.0 | 315 | 21 | US-09-760-446A-1779 | Sequence 1779, Ap |
| 41 | 103 | 100.0 | 325 | 1 | PCT-US01-14627-13008 | Sequence 13008, A |
| 42 | 97 | 94.2 | 168 | 3 | US-07-987-751-7 | Sequence 7, Appli |
| 43 | 95 | 92.2 | 170 | 3 | US-07-798-099-1 | Sequence 10, Appl |
| 44 | 92.5 | 89.8 | 169 | 3 | US-07-987-751-10 | Sequence 5529, Ap |
| 45 | 88.5 | 85.9 | 36 | 26 | US-60-196-710-5529 | |

ALIGNMENTS

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RESULT 1
US-09-813-383-1
; Sequence 1, Application US/09813383
; GENERAL INFORMATION:
; APPLICANT: WARREN, KENNETH G.
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS
; FILE REFERENCE: 0986810/027 8741
; CURRENT APPLICATION NUMBER: US/09/813, 383
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-813-383-1

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Query Match      100.0%; Score 103; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 4.le-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 8 HYGSLPQKSHGRTQDENP 25

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RESULT 2
US-09-760-443-1465
; Sequence 1465, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ212
; CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1465
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-443-1465

Query Match 100.0%; Score 103; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 18 HYGSLPQKSHGRTQDENP 35

RESULT 3
US-09-760-495-898
; Sequence 898, Application US/09760495
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC021
; CURRENT APPLICATION NUMBER: US/09/760,495
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1064
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 898
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-495-898

Query Match 100.0%; Score 103; DB 21; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 18 HYGSLPQKSHGRTQDENP 35

RESULT 4
US-09-760-443-1435
; Sequence 1435, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ212
; CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1435
; LENGTH: 136
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-443-1435

Query Match 100.0%; Score 103; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 95 HYGSLPQKSHGRTQDENP 112

RESULT 5
US-09-760-495-651
; Sequence 651, Application US/09760495
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC021
; CURRENT APPLICATION NUMBER: US/09/760,495
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1064
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 651
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (116)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-495-651

Query Match 100.0%; Score 103; DB 21; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 95 HYGSLPQKSHGRTQDENP 112

RESULT 6
US-07-987-751-3
; Sequence 3, Application US/07987751
; GENERAL INFORMATION:
; APPLICANT: Clark, Brian R.
; TITLE OF INVENTION: Methods for the Rapid Determination of
; Antigen-Specific T Cell Frequency
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,751
; FILING DATE: 19921204
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14058-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-987-751-3

Query Match 100.0%; Score 103; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 7
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; Sequence 4, Application US/07987751
; GENERAL INFORMATION:
; APPLICANT: Clark, Brian R.
; TITLE OF INVENTION: Methods for the Rapid Determination of
; Antigen-Specific T Cell Frequency
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,751
; FILING DATE: 19921204
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14058-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-987-751-4

Query Match 100.0%; Score 103; DB 3; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
| | | | | | | | | | | | | | | | | |
Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 8
US-07-798-099A-1
; Sequence 1, Application US/0798099A
; GENERAL INFORMATION:
; APPLICANT: WARREN, Kenneth G.
; APPLICANT: CATZ, Ingrid
; TITLE OF INVENTION: SYNTHETIC PEPTIDE SPECIFICITY OF
; ANTI-MYELIN BASIC PROTEIN FROM MULTIPLE SCLEROSIS
; CEREOSPINAL FLUID
; TITLE OF INVENTION: CEREOSPINAL FLUID
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robert M. Phipps
; STREET: 329 S. 9th Street
; CITY: Mayfield
; STATE: Kentucky
; COUNTRY: USA
; ZIP: 42066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/798,099A
; FILING DATE: 27-NOV-1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PHIPPS, Robert M.
; REGISTRATION NUMBER: 20,959
; REFERENCE/DOCKET NUMBER: A - 202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (502)247-9019
; TELEFAX: (502)247-9019
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
IMMEDIATE SOURCE:
CLONE: human myelin basic protein
US-07-798-099A-1

Query Match 100.0%; Score 103; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
|||||

Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 9
US-08-241-246-I
; Sequence 1. Application US/08241246
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn;
; APPLICANT: Hsu, Di-Hwei; and
; APPLICANT: Shi, Jia-Dong.
; TITLE OF INVENTION: COMPOSITIONS AND TREATMENT FOR MULTIPLE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State street, suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241.246
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006.116
; FILING DATE: 15-JANUARY-1993
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-053 (084.00S)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-241-246-1

Query Match 100.0%; Score 103; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 2e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYGSLPQKSHGRTQDENP 18
|||||

Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 10
US-08-241-246B-1
; Sequence 1. Application US/08241246B
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn; Hsu, Di-Hwei; and Shi, Jia-Dong
; TITLE OF INVENTION: COMPOSITIONS AND TREATMENT FOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241.246B
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006.116
; FILING DATE: 15-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-053 (084.00S)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-241-246B-I

Query Match 100.0%; Score 103; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
|||||

Db 68 HYGSLPQKSHGRTQDENP 85

RESULT 11
US-08-327-357-1
; Sequence 1. Application US/08327357
; GENERAL INFORMATION:
; APPLICANT: WARREN, Kenneth G.
; APPLICANT: CATZ, Ingrid
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN
; BASIC PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC
; PROTEIN PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W.

```

; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3917
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/327,357
; FILING DATE: 21-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CA 2,053,799-0
; FILING DATE: 22-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Jeffrey L. Ihnen
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 18760-95536(temp)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)962-4800
; TELEFAX: (202)962-8300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; IMMEDIATE SOURCE:
; CLONE: human myelin basic protein
; US-08-327-357-1

Query Match 100.0%; Score 103; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18
Db 68 HYGSLPKSHGRTQDENP 85

RESULT 12
US-08-328-224-5
; Sequence 5, Application US/08328224
; GENERAL INFORMATION:
; APPLICANT: Smilek, Dawn
; APPLICANT: Samson, Michael
; APPLICANT: Gefter, Malcolm
; APPLICANT: Hsu, Di-Hwei
; APPLICANT: Shi, Jia-Doug
; APPLICANT: Paliard, Xavier
; APPLICANT: Devaux, Brigitte
; APPLICANT: Rothbard, Jonathan
; APPLICANT: Franzen, Henry M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING TO HUMANS SUPPERIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,224
; FILING DATE: 10-25-94
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 094.0 US (IMI-056)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-328-224-5

Query Match 100.0%; Score 103; DB 7; Length 170;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18
Db 68 HYGSLPKSHGRTQDENP 85

RESULT 13
US-08-342-078-2
; Sequence 2, Application US/08342078
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ling, Nicholas
; APPLICANT: Conlon, Paul J.
; APPLICANT: Gaur, Amitabh
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
; TITLE OF INVENTION: SCLEROSIS USING PEPTIDE ANALOGUES AT POSITION 91 OF HUMAN
; TITLE OF INVENTION: MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,078
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Nottenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 690068.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-342-078-2

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Query Match 100.0%; Score 103; DB 7; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18
 |||||

Db 68 HYGSLPKSHGRTQDENP 85

RESULT 14

US-08-404-228-1

; sequence 1, Application US/08404228

; GENERAL INFORMATION:

; APPLICANT: Smilek, Dawn;

; APPLICANT: Samson, Michael F.;

; APPLICANT: Geffer, Malcolm;

; APPLICANT: Hsu, Di-Hwei;

; APPLICANT: Shi, Jia-Dong;

; APPLICANT: Pallard, Xavier;

; APPLICANT: Devaux, Brigitte;

; APPLICANT: Rothbard, Jonathan;

; APPLICANT: Franzen, Henry M.

; TITLE OF INVENTION: Compositions and Treatment for Multiple

; NUMBER OF SEQUENCES: 71

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/404,228

; FILING DATE: 15-March-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Anne I. Craig

; REGISTRATION NUMBER: Reg. No. 32, 976

; REFERENCE/DOCKET NUMBER: 094.1 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 466-6000

; TELEFAX: (617) 466-6010

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-404-228-1

Query Match 100.0%; Score 103; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPKSHGRTQDENP 18
 |||||

Db 68 HYGSLPKSHGRTQDENP 85

RESULT 15

US-08-462-941A-1

; sequence 1, Application US/08462941A

; GENERAL INFORMATION:

; APPLICANT: Smilek, Dawn;

; APPLICANT: Samson, Michael F.;

; APPLICANT: Geffer, Malcolm;

; APPLICANT: Hsu, Di-Hwei;

; APPLICANT: Shi, Jia-Dong;

; APPLICANT: Pallard, Xavier;

; APPLICANT: Devaux, Brigitte;

; APPLICANT: Rothbard, Jonathan; and

; APPLICANT: Franzen, Henry M.

; TITLE OF INVENTION: Compositions and Treatment for Multiple

; NUMBER OF SEQUENCES: 71

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,941A

; FILING DATE: 5-June-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/404,228

; FILING DATE: 15-March-1995

; APPLICATION NUMBER: US 08/328,224

; FILING DATE: 25-October-1994

; APPLICATION NUMBER: US 08/300,811

; FILING DATE: 1-September-1994

; APPLICATION NUMBER: US 08/241,246

; FILING DATE: 10-May-1994

; APPLICATION NUMBER: US 08/116,824

; FILING DATE: 3-September-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Amy E. Mandragouras

; REGISTRATION NUMBER: Reg. No. 36,207

; REFERENCE/DOCKET NUMBER: 094.1 USD1 (IMI-052CPDV)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-462-941A-1

Query Match 100.0%; Score 103; DB 8; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HYGSLPKSHGRTQDENP 18
 |||||

Db 68 HYGSLPKSHGRTQDENP 85

Search completed: August 28, 2002, 16:39:34
 Job time: 346 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:40:33 ; Search time 53.03 Seconds
(without alignments)
82.159 Million cell updates/sec

Title: US-09-813-383-1_COPY_8_25
Perfect score: 103
Sequence: 1 HYGSLPKSHGRTQDENP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747981 seqs, 242050750 residues

Total number of hits satisfying chosen parameters: 747981

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 103 | 100.0 | 46 | 5 | US-09-813-463A-1 |
| 2 | 103 | 100.0 | 108 | 6 | US-10-143-775-898 |
| 3 | 103 | 100.0 | 108 | 6 | US-10-212-054-1465 |
| 4 | 103 | 100.0 | 136 | 6 | US-10-143-775-651 |
| 5 | 103 | 100.0 | 136 | 6 | US-10-212-054-1435 |
| 6 | 103 | 100.0 | 171 | 1 | PCT-US02-13527-12 |
| 7 | 103 | 100.0 | 171 | 6 | US-10-104-973-2 |
| 8 | 103 | 100.0 | 172 | 4 | US-08-431-644B-4 |
| 9 | 103 | 100.0 | 172 | 4 | US-08-431-644C-4 |
| 10 | 103 | 100.0 | 197 | 4 | US-08-431-644B-1 |
| 11 | 103 | 100.0 | 197 | 4 | US-08-431-644C-1 |
| 12 | 103 | 100.0 | 203 | 4 | US-08-431-644B-2 |
| 13 | 103 | 100.0 | 203 | 4 | US-08-431-644B-3 |
| 14 | 103 | 100.0 | 203 | 4 | US-08-431-644B-27 |
| 15 | 103 | 100.0 | 203 | 4 | US-08-431-644C-2 |
| 16 | 103 | 100.0 | 203 | 4 | US-08-431-644C-3 |
| 17 | 103 | 100.0 | 203 | 4 | US-08-431-644C-27 |
| 18 | 103 | 100.0 | 315 | 6 | US-10-206-664-1779 |
| 19 | 103 | 100.0 | 315 | 6 | US-10-212-054-1502 |
| 20 | 82 | 79.6 | 15 | 5 | US-09-813-463A-6 |
| 21 | 67 | 65.0 | 20 | 5 | US-09-906-206A-34 |
| 22 | 67 | 65.0 | 20 | 5 | US-09-715-708A-35 |
| 23 | 66.5 | 64.6 | 17 | 1 | PCT-US02-00337-1 |
| 24 | 64 | 62.1 | 15 | 5 | US-09-813-463A-4 |
| 25 | 63.5 | 61.7 | 19 | 1 | PCT-US02-13873-30 |
| 26 | 62 | 60.2 | 21 | 5 | US-09-813-463A-3 |

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27 59.5 57.8 19 1 PCT-US02-13873-25 Sequence 25, Appl
28 49.5 48.1 37 1 PCT-US02-13873-4 Sequence 4, Appli
29 47.5 46.1 987 5 US-09-935-625-6080 Sequence 6080, Ap
30 47.5 46.1 987 5 US-09-935-625-14260 Sequence 14260, Ap
31 47.5 46.1 987 5 US-09-935-625-23047 Sequence 23047, A
32 47.5 46.1 987 5 US-09-935-625-26918 Sequence 26918, A
33 47.5 46.1 994 5 US-09-935-625-60799 Sequence 6079, Ap
34 47.5 46.1 994 5 US-09-935-625-14259 Sequence 14259, A
35 47.5 46.1 994 5 US-09-935-625-23046 Sequence 23046, A
36 47.5 46.1 994 5 US-09-935-625-26917 Sequence 26917, A
37 47.5 46.1 1123 5 US-09-935-625-6078 Sequence 6078, Ap
38 47.5 46.1 1123 5 US-09-935-625-14258 Sequence 14258, A
39 47.5 46.1 1123 5 US-09-935-625-23045 Sequence 23045, A
40 47.5 46.1 1123 5 US-09-935-625-26916 Sequence 26916, A
41 46 44.7 15 5 US-09-813-463A-5 Sequence 5, Appli
42 46 44.7 230 7 US-60-360-039-2545 Sequence 2545, Ap
43 45 43.7 23 5 US-09-906-206A-8 Sequence 8, Appli
44 45 43.7 23 5 US-09-715-708A-1 Sequence 1, Appli
45 45 43.7 24 5 US-09-707-738-2 Sequence 2, Appli

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ALIGNMENTS

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RESULT 1
US-09-813-463A-1
; Sequence 1, Application US/09813463A
; GENERAL INFORMATION:
; APPLICANT: WARREN, KENNETH G.
; APPLICANT: CATZ, INGRID
; TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN AND
; TITLE OF INVENTION: THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO
; TITLE OF INVENTION: MULTIPLE SCLEROSIS PATIENTS
; FILE REFERENCE: 098810/027 8740
; CURRENT APPLICATION NUMBER: US/09/813,463A
; CURRENT FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-813-463A-1

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Query Match 100.0%; Score 103; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HYGSLPKSHGRTQDENP 18
Db 8 HYGSLPKSHGRTQDENP 25

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RESULT 2
US-10-143-775-898
; Sequence 898, Application US/10143775
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC021C1N
; CURRENT APPLICATION NUMBER: US/10/143,775
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1064
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 898
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-143-775-898

Query Match 100.0%; Score 103; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
|||||

Db 18 HYGSLPQKSHGRTQDENP 35

RESULT 3

US-10-212-054-1465

; Sequence 1465, Application US/10212054

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJ212C1N

; CURRENT APPLICATION NUMBER: US/10/212,054

; CURRENT FILING DATE: 2002-08-06

; NUMBER OF SEQ ID NOS: 2164

; Prior application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1465

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-212-054-1465

Query Match 100.0%; Score 103; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
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Db 18 HYGSLPQKSHGRTQDENP 35

RESULT 4

US-10-143-775-651

; Sequence 651, Application US/10143775

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC021C1N

; CURRENT APPLICATION NUMBER: US/10/143,775

; CURRENT FILING DATE: 2002-05-14

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 1064

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 651

; LENGTH: 136

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (113)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: misc_feature

; LOCATION: (116)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (117)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (124)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (124)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-143-775-651

Query Match 100.0%; Score 103; DB 6; Length 136;
Best Local Similarity 100.0%; Pred. No. 8.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
|||||

Db 95 HYGSLPQKSHGRTQDENP 112

RESULT 5

US-10-212-054-1435

; Sequence 1435, Application US/10212054

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJ212C1N

; CURRENT APPLICATION NUMBER: US/10/212,054

; CURRENT FILING DATE: 2002-08-06

; NUMBER OF SEQ ID NOS: 2164

; Prior application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1435

; LENGTH: 136

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (113)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (116)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (117)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (124)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (127)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (136)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-212-054-1435

Query Match 100.0%; Score 103; DB 6; Length 136;
Best Local Similarity 100.0%; Pred. No. 8.8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
|||||

Db 95 HYGSLPQKSHGRTQDENP 112

RESULT 6

PCT-US02-13527-12

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; Sequence 12, Application PCT/US0213527
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoheng
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004QPC
; CURRENT APPLICATION NUMBER: PCT/US02/13527
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US 10/000,439
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-13527-12
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Query Match 100.0%; Score 103; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.le-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HYGSLPOKSHGRQTQDENP 18
| | | | | | | | | | | | | | | | | |
Db 69 HYGSLPOKSHGRQTQDENP 86
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```
RESULT 7
US-10-104-973-2
; Sequence 2, Application US/10104973
; GENERAL INFORMATION:
```

```
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C4
; CURRENT APPLICATION NUMBER: US/10/104,973
; CURRENT FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-973-2
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```
Query Match 100.0%; Score 103; DB 6; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.le-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HYGSLPOKSHGRQTQDENP 18
| | | | | | | | | | | | | | | | | |
Db 69 HYGSLPOKSHGRQTQDENP 86
```

```
RESULT 8
US-08-431-644B-4
; Sequence 4, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
```

```
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644B
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: human
; US-08-431-644B-4
```

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Query Match 100.0%; Score 103; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.le-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HYGSLPOKSHGRQTQDENP 18
| | | | | | | | | | | | | | | | | |
Db 70 HYGSLPOKSHGRQTQDENP 87
```

```
RESULT 9
US-08-431-644C-4
; Sequence 4, Application US/08431644C
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1087-48(27)
; CURRENT APPLICATION NUMBER: US/08/431,644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: human
; US-08-431-644C-4
```

```
Query Match 100.0%; Score 103; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.le-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HYGSLPOKSHGRQTQDENP 18
| | | | | | | | | | | | | | | | | |
Db 70 HYGSLPOKSHGRQTQDENP 87
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```
RESULT 10
US-08-431-644B-1
; Sequence 1, Application US/08431644B
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Lenardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
```

```

1 // Sequence 27, Application US/08431644B
2 //
3 // GENERAL INFORMATION:
4 //
5 // APPLICANT: Nye, Steven H.
6 // APPLICANT: Lenardo, Michael J.
7 // APPLICANT: McFarland, Henry F.
8 // APPLICANT: Matis, Louis A.
9 // APPLICANT: Mueller, Eileen E.
10 // APPLICANT: Mueller, John P.
11 // APPLICANT: Pelfrey, Clara M.
12 // APPLICANT: Squinto, Stephen P.
13 // APPLICANT: Wilkins, James A.
14 //
15 // TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
16 //
17 // FILE REFERENCE: 1087-48(27)
18 // CURRENT APPLICATION NUMBER: US/08/431.644B
19 // CURRENT FILING DATE: 1995-05-02

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Thu Aug 29 10:03:57 2002

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644B-27

Query Match 100.0%; Score 103; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

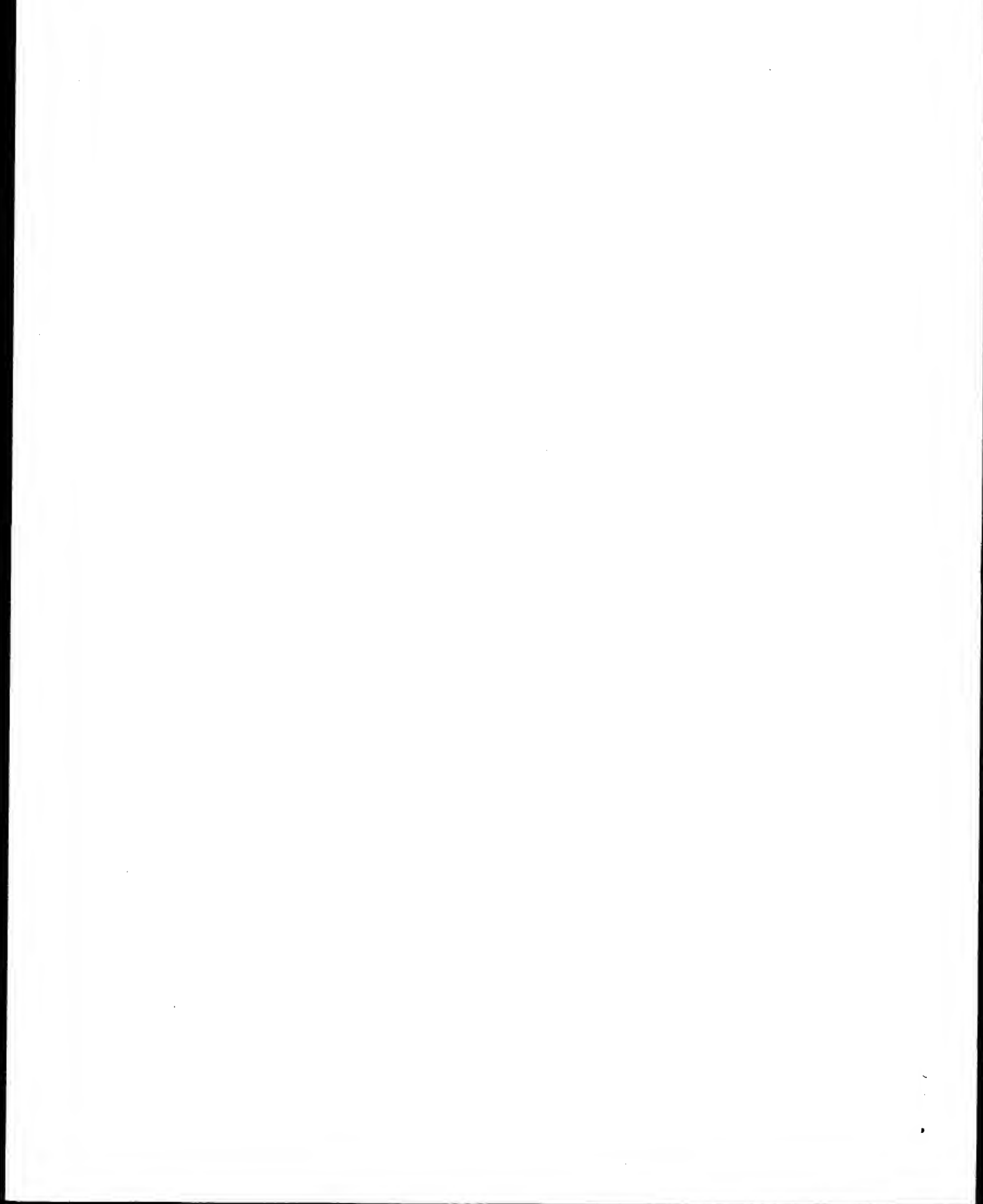
QY 1 HYGSLPQKSHGRTQDENP 18
Db 95 HYGSLPQKSHGRTQDENP 112

RESULT 15
US-08-431-644C-2
; Sequence 2. Application US/08431644C
; GENERAL INFORMATION:
; APPLICANT: Nye, Steven H.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen E.
; APPLICANT: Mueller, John P.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: MODIFIED MYELIN BASIC PROTEIN MOLECULES
; FILE REFERENCE: 1067-48(27)
; CURRENT APPLICATION NUMBER: US/08/431.644C
; CURRENT FILING DATE: 1995-05-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: human
US-08-431-644C-2

Query Match 100.0%; Score 103; DB 4; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
Db 95 HYGSLPQKSHGRTQDENP 112

Search completed: August 28, 2002, 16:40:34
Job time: 386 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:36:03 ; Search time 25.27 Seconds
(without alignments)
68.445 Million cell updates/sec

Title: US-09-813-383-1-copy_8_25

Perfect score: 103

Sequence: 1 HYGSLPQKSHGRQTQDENP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB Seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.71.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 103 | 100.0 | 197 | 1 MBHUB | myelin basic prote |
| 2 | 92.5 | 89.8 | 328 | 1 MBWSB | golfi-myelin basic |
| 3 | 85 | 82.5 | 171 | 1 MBGZB | myelin basic prote |
| 4 | 83.5 | 81.1 | 171 | 1 MBPGB | myelin basic prote |
| 5 | 79 | 76.7 | 42 | 2 B92087 | myelin basic prote |
| 6 | 78.5 | 76.2 | 128 | 1 MBPTS | myelin basic prote |
| 7 | 75.5 | 73.3 | 169 | 1 MBBOB | myelin basic prote |
| 8 | 74.5 | 72.3 | 167 | 2 A37246 | myelin basic prote |
| 9 | 63.5 | 61.7 | 174 | 2 S08535 | myelin basic prote |
| 10 | 48 | 46.6 | 333 | 2 T35894 | hypothetical prote |
| 11 | 46 | 44.7 | 230 | 2 S41043 | ruml protein - fis |
| 12 | 46 | 44.7 | 230 | 2 T40233 | Rumlp - fission ye |
| 13 | 46 | 44.7 | 257 | 2 D82350 | Ribonuclease PH VC |
| 14 | 46 | 44.7 | 632 | 2 F83387 | copper resistance |
| 15 | 45 | 43.7 | 238 | 1 A64059 | tRNA nucleotidyltr |
| 16 | 44 | 42.7 | 237 | 2 E90476 | hypothetical prote |
| 17 | 44 | 42.7 | 295 | 2 S58850 | homeotic protein a |
| 18 | 44 | 42.7 | 497 | 1 A29055 | aldohyde dehydroge |
| 19 | 43 | 41.7 | 366 | 2 JC7690 | Gfi-1-like protein |
| 20 | 42 | 40.8 | 241 | 2 C82673 | Ribonuclease PH XF |
| 21 | 42 | 40.8 | 316 | 2 D83233 | hypothetical prote |
| 22 | 42 | 40.8 | 491 | 2 A9179 | melanoma antigen h |
| 23 | 42 | 40.8 | 2531 | 2 T31070 | notch homolog - se |
| 24 | 41 | 39.8 | 115 | 2 T26191 | hypothetical prote |
| 25 | 41 | 39.8 | 168 | 2 A39316 | RAB-17 protein - m |
| 26 | 41 | 39.8 | 168 | 2 S08633 | RAB-17 protein - m |
| 27 | 41 | 39.8 | 205 | 2 F87560 | Ribosomal protein |
| 28 | 41 | 39.8 | 254 | 2 C82868 | plasmid replicatio |
| 29 | 41 | 39.8 | 340 | 2 F33282 | DNA-binding protei |

ALIGNMENTS

RESULT 1

MBHUB

myelin basic protein [validated] - human

N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein p

.5K splice form

C:Species: Homo sapiens (man)

C:Date: 18-Dec-1981 #sequence_revision 25-Aug-1995 #text_change 20-Apr-2001

C:Accession: S10482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219;

R:Streichler, R.; Stoffel, W.

Biol. Chem. Hoppe-Seyler 370, 503-510, 1989

A:Title: The organization of the human myelin basic protein gene. Comparison with the

A:Reference number: S10482; MUID:89302693

A:Accession: S10482

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-197 <STR>

A:CROSS-references: EMBL:X17286; NID:g34490; PIDN:CAA35179.1; PID:g1184244

R:Kamholz, J.; De Ferra, F.; Puckett, C.; Lazzarini, R.

Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986

A:Title: Identification of three forms of human myelin basic protein by cDNA cloning.

A:Reference number: A94106; MUID:86259714

A:Accession: A94106

A:Molecule type: mRNA

A:Residues: 1-39,86-197 <RAM>

A:CROSS-references: GB:M13577; NID:g187408; PIDN:AAA59562.1; PID:g307160

A:Note: 18.5K splice form

A:Accession: B94106

A:Molecule type: mRNA

A:Residues: 1-197 <KA2>

A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form

A:Note: a 17.2K splice form is also described

A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K

R:Carnegele, P.R.

Biochem. J. 123, 57-67, 1971

A:Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.

A:Reference number: A90256; MUID:72066400

A:Accession: A90256

A:Molecule type: protein

A:Residues: 2-59,86-197 <CAR>

R:Proost, P.; Van Damme, J.; Opdenakker, G.

Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993

A:Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin b

A:Reference number: JH0802; MUID:93282820

A:Accession: JH0802

A:Molecule type: protein

A:Residues: 2-59,86-197 <PRO>

A:Experimental source: brain

R:Scoble, H.A.; Whitaker, J.N.; Biemann, K.

J. Neurochem. 47, 614-616, 1986

A:Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44

A:Reference number: A60862; MUID:86280476

A:Accession: A60862

probable portal pr
protoplast regene
exodeoxyribonuclea
DNA helicase RecB
DNA helicase RecB
ataxin-2 - mouse
liver stage antige
ALR protein - huma
ALR protein - huma
ribonuclease famil
ribonuclease famil
superoxide dismuta
ribosomal protein
ribosomal protein
tRNA nucleotidyltr
hypothetical prote

30 41 39.8 554 2 A91250
31 41 39.8 932 2 S62555
32 41 39.8 1180 1 NCECX5
33 41 39.8 1180 2 E91088
34 41 39.8 1180 2 G85933
35 41 39.8 1285 2 T14171
36 41 39.8 1909 2 A45592
37 41 39.8 4957 2 T03455
38 41 39.8 5262 2 T03454
39 40.5 39.3 676 2 B72071
40 40.5 39.3 676 2 D86553
41 40 38.8 152 2 S72235
42 40 38.8 188 1 R5XL8A
43 40 38.8 188 1 R5XL14
44 40 38.8 238 2 AE0006
45 40 38.8 390 2 T46028

A:Molecule type: protein
A:Residues: 2-45,117-197 <SCQ>
A:Note: evidence for acetylated amino end
R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Biemann, K.
J. Biol. Chem. 259, 5028-5031, 1984
A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by mass spectrometry
A:Reference number: A61420; MUID:84185608
A:Accession: A61420
A:Molecule type: protein
A:Residues: 46-59,86-116 <GIB>
R:Wood, D.D.; Moscarello, M.A.
J. Biol. Chem. 264, 5121-5127, 1989
A:Title: The isolation, characterization, and lipid-aggregating properties of a citrulline-rich myelin basic protein peptide
A:Reference number: A33273; MUID:89174797
A:Accession: A33273
A:Molecule type: protein
A:Residues: 15-25,'X',27-31,'X',33-59,86-148,'X',150-156,'X',158-185,'X',187-196,'X' <WC>
R:Baldwin, G.S.; Carnegie, P.R.
Biochem. J. 123, 69-74, 1971
A:Title: Isolation and partial characterization of methylated arginines from the encephalomyelinase-sensitive fraction of bovine brain
A:Reference number: A90257; MUID:72066401
A:Contents: annotation; methylarginine
A:Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approx 100% of the total arginines
R:Lennon, V.A.; Wilks, A.V.; Carnegie, P.R.
J. Immunol. 105, 1223-1230, 1970
A:Reference number: A92806; MUID:71088405
A:Contents: annotation
A:Note: a region including residues 139-149 induces experimental autoimmune encephalomyelitis in mice
R:Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prusiner, S.B.
Genomics 6, 16-22, 1990
A:Title: Repetitive DNA (TGGAG)n 5' to the human myelin basic protein gene: a new form of myelin basic protein gene
A:Reference number: I54219; MUID:90152679
A:Accession: I54219
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-59 <RES>
A:Cross-references: GB:M63599; NID:g187402; PIDN:AAA59560.1; PID:g187403
R:Roth, H.J.; Kronquist, K.; Kerleto de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 17, 321-328, 1987
A:Title: Evidence for the expression of four myelin basic protein variants in the developing mouse brain
A:Reference number: I56567; MUID:87311781
A:Accession: I56567
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-132,144-197 <RE2>
A:Cross-references: GB:M30516; NID:g187410; PIDN:AAA59563.1; PID:g307161
A:Accession: I73634
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-197 <RE3>
A:Cross-references: GB:M30515; NID:g187412; PIDN:AAA59564.1; PID:g307162
R:Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 16, 227-238, 1986
A:Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin basic protein
A:Reference number: I56565; MUID:86308101
A:Accession: I56565
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-59,86-113,145-197 <RE4>
A:Cross-references: GB:M30047; NID:g187400; PIDN:AAA59559.1; PID:g307159
R:Boulias, C.; Pang, H.; Mastronardi, F.; Moscarello, M.A.
Arch. Biochem. Biophys. 322, 174-182, 1995
A:Title: The isolation and characterization of four myelin basic proteins from the unbound fraction of bovine brain
A:Reference number: S66383; MUID:96004793
A:Accession: S66383
A:Molecule type: protein
A:Residues: 23-25,'X',27-39 <BOU>
A:Comment: Four alternatively spliced forms of myelin basic protein have been observed, C, D, E, and F
A:Gene: GDB:MBP
A:Cross-references: GDB:I19379; OMIM:159430
A:Map position: 18q22-18qter

A:Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
C:Description: probably helps maintain myelin structure
C:Superfamily: myelin basic protein
C:Keywords: acetylated amino end; alternative splicing; citrulline; experimental auto
F:2-137/Product: myelin basic protein, 21.5K splice form #status predicted <WAT>
F:2-132,144-197/Product: myelin basic protein, 20.2K splice form #status predicted <WAT>
F:2-59,86-197/Product: myelin basic protein, 18.5K splice form #status experimental <WAT>
F:2-59,86-132,144-197/Product: myelin basic protein, 18.5K splice form #status experimental <WAT>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:28,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experimental
F:134/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)
Query Match 100.0%; Score 103; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 9.5e-10; Mismatches 0; Gaps 0;
Matches 18; Conservative 0; Indels 0;
QY 1 HYGSLPQKSHGRQTQDENP 18
Db 95 HYGSLPQKSHGRQTQDENP 112
|||||
RESULT 2
MBMSB
golli-myelin basic protein precursor - mouse
N:Alternate names: golli-mbp protein; MBP
N:Contains: myelin basic protein
C:Species: Mus musculus (house mouse)
C>Date: 17-Mar-1987 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
R:Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Land
J. Biol. Chem. 268, 4930-4938, 1993
A:Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene the
A:Reference number: A45421; MUID:93186801
A:Accession: A45421
A:Molecule type: mRNA
A:Residues: 1-190;217-276;316-328 <CAM>
A:Cross-references: GB:L07508; NID:gl93586; PIDN:AAA37721.1; PID:g193587
A:Experimental source: clone BG21
A:Note: sequence extracted from NCBI backbone (NCBI:126700, NCBI:126715)
R:de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molineaux, S.; Lazzar
Cell 43, 721-727, 1985
A:Title: Alternative splicing accounts for the four forms of myelin basic protein.
A:Reference number: A90875; MUID:86079555
A:Accession: A90875
A:Molecule type: mRNA
A:Residues: 1-191,'SSBP' <CAM2>
A:Cross-references: GB:L07508; NID:gl93586; PIDN:AAA37721.1; PID:g193587
A:Experimental source: clone BG21
A:Note: sequence extracted from NCBI backbone (NCBI:126700, NCBI:126715)
R:de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molineaux, S.; Lazzar
Cell 43, 721-727, 1985
A:Title: Alternative splicing accounts for the four forms of myelin basic protein.
A:Reference number: A90875; MUID:86079555
A:Accession: A90875
A:Molecule type: mRNA
A:Residues: 134-328 <DEF>
A:Cross-references: GB:L00404; GB:M11669; NID:gl99060; PIDN:AAA39502.1; PID:g387419
A:Experimental source: 21.5K
R:Takahashi, N.; Roach, A.; Teplow, D.B.; Prusiner, S.B.; Hood, L.
Cell 42, 139-148, 1985
A:Title: Cloning and characterization of the myelin basic protein gene from mouse: on
A:Reference number: A90867; MUID:85254913
A:Accession: A90867
A:Molecule type: DNA
A:Residues: 134-190;217-328 <TAK>
A:Cross-references: GB:M11533; NID:gl99044; PIDN:AAA39496.1; PID:g387414
A:Experimental source: 18.5K
R:Newman, S.; Kitamura, K.; Campagnoni, A.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987
A:Title: Identification of a cDNA coding for a fifth form of myelin basic protein in
A:Reference number: A94188; MUID:87118269
A:Accession: A26591
A:Molecule type: mRNA

Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 HYGSLPQKS-HGRTQDENP 18
|||||
Db 224 HYGSLPQKSQHGRQDENP 242
|||||

RESULT 3
MBCZB
myelin basic protein - chimpanzee (tentative sequence)
N:Alternate names: MBP
C:Species: Pan troglodytes (chimpanzee)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 06-Sep-1996
C:Accession: A03139
R:Westall, F.C.; Thompson, M.; Kalter, S.S.
Life Sci. 17, 219-223, 1975
A:Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.
A:Reference number: A03139; MUID:76009821
A:Accession: A03139
A:Molecule type: protein
A:Residues: 1-171 <WES>
C:Comment: This protein may function in maintaining the proper structure of myelin.
C:Superfamily: myelin basic protein
C:Keywords: blocked amino end; methylated amino acid; myelin; structural protein
F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
F:107/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

Query Match 82.5%; Score 85; DB 1; Length 171;
Best Local Similarity 88.9%; Pred. No. 8.7e-07;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGSLPQKS-HGRTQDENP 18
|||||
Db 68 HYGSLPQKS-HGRTQDENP 85
|||||

RESULT 4
MBPGB
myelin basic protein - pig (tentative sequence)
N:Alternate names: myelin A1 protein
C:Contains: myelin basic protein amide 14
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Apr-1996 #sequence_revision 26-Apr-1996 #text_change 07-May-1999
C:Accession: A61640; A36245
R:Kira, J.; Deibler, G.E.; Krutzsch, H.C.; Martenson, R.E.
J. Neurochem. 44, 134-142, 1985
A:Title: Amino acid sequence of porcine myelin basic protein.
A:Reference number: A61640; MUID:85056964
A:Accession: A61640
A:Molecule type: protein
A:Residues: 1-171 <KIR>
A:Note: some peptides were ordered by homology
R:Takamatsu, K.; Tatamoto, K.
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.
A:Reference number: A36245; MUID:91058553
A:Accession: A36245
A:Molecule type: protein
A:Residues: 1-14 <TAK>
A:Note: the peptide in the abstract is inconsistent with that in figure 3 in having
A:Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymatic
C:Superfamily: myelin basic protein
C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis
F:1-171/Product: myelin basic protein #status experimental <MAT>
F:1-14/Product: myelin peptide amide-14 #status experimental
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:14/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide
F:107/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

Query Match 81.1%; Score 83.5; DB 1; Length 171;
Best Local Similarity 84.2%; Pred. No. 1.6e-06;

A:Residues: 134-274; 316-328 <NEW1>
A:Cross-references: GB:M15060; NID:g199048; PIDN:AA59711.1; PID:g199049
A:Experimental source: clone M722; splice form 17.22K
A:Accession: B26591
A:Molecule type: mRNA
A:Residues: 134-190; 217-263; 275-328 <NEW2>
A:Cross-references: GB:M15062; NID:g199050
A:Experimental source: clone M78; splice form 17.24K
R:Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V.W.
J. Neurochem. 54, 2032-2041, 1990
A:Title: Expression of a novel transcript of the myelin basic protein gene.
A:Reference number: A60920; MUID:90250449
A:Accession: A60920
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 134-190; 217-274; 316-328 <KIT>
A:Experimental source: M41; splice form 14K
R:Grima, B.; Zelenika, D.; Pessac, B.
J. Neurochem. 59, 2318-2323, 1992
A:Title: A novel transcript overlapping the myelin basic protein gene.
A:Reference number: I48407; MUID:93057537
A:Accession: I48407
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-191, 'SSEP' <GRI>
A:Cross-references: EMBL:X67319; NID:g51332; PIDN:CAA47733.1; PID:g51333
A:Note: submitted to the EMBL Data Library, July 1992
R:Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984
A:Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin basic
A:Reference number: I58996; MUID:84119431
A:Accession: I58996
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 219-248 <ZEL>
A:Cross-references: GB:R00989; NID:g199037; PIDN:AAA39495.1; PID:g554195
R:Miura, M.; Tamura, T.
Gene 75, 31-38, 1989
A:Title: The promoter elements of the mouse myelin basic protein gene function efficiently
A:Reference number: I54033; MUID:89252919
A:Accession: I54033
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 134-157 <MIU>
A:Cross-references: GB:M24410; NID:g199052; PIDN:AAA39498.1; PID:g554196
R:Okano, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.
EMBO J. 7, 77-83, 1988
A:Title: Gene organization and transcription of duplicated MBP genes of myelin deficient
A:Reference number: I53256; MUID:88196094
A:Accession: I53256
A:Status: translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 217-229, 'HN' 232-250 <OKA>
A:Cross-references: GB:M36275; NID:g199069; PIDN:AAA39504.1; PID:g293725
A:Note: hypothetical translation of the reversed and complementary sequence to that shown
C:Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K, 17.22K and
C:Genetics:
A:Gene: Golli-mbp; shi-mld
A:Introns: 190/3; 250/3; 262/3; 273/3; 314/3
C:Function:
A:Description: probably helps maintain myelin structure
C:Superfamily: myelin basic protein
C:Keywords: alternative splicing; myelin; structural protein
F:1-190, 217-276, 316-328/Product: Golli-mbp protein (clone J37) #status predicted <MAL>
F:134-328/Product: myelin basic protein, splice form 21.5K #status predicted <WAT>
F:134-274, 316-328/Product: myelin basic protein, splice form 17K-a #status predicted <WA>
F:134-190, 217-328/Product: myelin basic protein, splice form 18.5K #status predicted <WA>
F:134-190, 217-263, 275-328/Product: myelin basic protein, splice form 17K-b #status predicted
F:134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predicted

Query Match 89.8%; Score 92.5; DB 1; Length 328;
Best Local Similarity 94.7%; Pred. No. 9.8e-08;

A: Note: These peptides have carboxyl-terminal amides probably produced by a non-enzymic reaction. A: Brostoff, S.; Eylar, E. H. *Proc. Natl. Acad. Sci. U.S.A.* 68, 765-769, 1971
 A: Title: Localization of methylated arginine in the A1 protein from myelin.
 A: Reference number: A93777; PMID:71153946
 A: Contents: annotation
 A: Note: Arg-106 is modified to monomethylarginine and dimethylarginine
 A: Eylar, E. H.; Caccam, J.; Jackson, J. J.; Westall, F. C.; Robinson, A. B. *Science* 168, 1220-1223, 1970
 A: Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site

A:Reference number: A94241; MUID:70178977

A:Contents: annotation
A:Note: the region including residues 114-122 induces experimental allergic encephalomyelitis in mice.
C:Superfamily: myelin basic protein
C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephalomyelitis; myelin basic protein #status experimental <MAT>
F:1-169/Product: myelin basic protein #status experimental <MAT>
F:1-16/Product: myelin peptide amide-16 #status experimental <PA16>
F:1-12/Product: myelin peptide amide-12 #status experimental <PA12>
F:1-12/Product: myelin peptide amide-12 #status experimental <PA12>
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide amide)
F:16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide amide)
F:106/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg) (C-terminal)

Query Match 73.3%; Score 75.5; DB 1; Length 169;
Best Local Similarity 78.9%; Pred. No. 3.4e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 HYGSLPQKSHG-RTQDENP 18
|||||||:|:|:|:|:|:|
Db 66 HYGSLPQKSHG-RTQDENP 84

RESULT 8

A37246
myelin basic protein - guinea pig
N:Alternate names: myelin Al protein
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 07-Oct-1994
C:Accession: A37246; C92087; A03140
R:Deliber, G.E.; Martenson, R.E.; Krutzsch, H.C.; Kies, M.W.
J. Neurochem. 43, 100-105, 1984
A:Title: Sequence of guinea pig myelin basic protein.
A:Reference number: A37246; MUID:84215086
A:Accession: A37246
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-167 <DE>
R:Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
J. Biol. Chem. 246, 4630-4640, 1971
A:Title: Encephalogenic fragment of myelin basic protein. Amino acid sequence of bovine myelin basic protein.
A:Reference number: A92087
A:Accession: C92087
A:Molecule type: protein
A:Residues: 45-87 <SHA>
C:Superfamily: myelin basic protein
C:Keywords: myelin

Query Match 72.3%; Score 74.5; DB 2; Length 167;
Best Local Similarity 83.3%; Pred. No. 5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGSLPQKSHGRTQDENP 18
|||||||:|:|:|:|:|:|
Db 68 HYGSLPQKSHGRTQDENP 84

RESULT 9

S08535
myelin basic protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 13-Aug-1999
C:Accession: S08535
R:Zopf, D.; Sonntag, V.; Betz, H.; Gundelfinger, E.D.
Glia 2, 241-249, 1989
A:Title: Developmental accumulation and heterogeneity of myelin basic protein transcripts in the developing chicken brain.
A:Reference number: S08535; MUID:89358239
A:Accession: S08535
A:Molecule type: mRNA
A:Residues: 1-174 <ZOP>
A:Cross-references: EMBL:X17103; NID:g63594; PIDN:CAA34959.1; PID:g63595
C:Superfamily: myelin basic protein

Query Match 61.7%; Score 63.5; DB 2; Length 174;
Best Local Similarity 63.2%; Pred. No. 0.0037;
Matches 12; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 HYGSLPQKSHGRTQDENP 18
|||||||:|:|:|:|:|:|
Db 66 HYGSLPQKSHGRTQDENP 84

RESULT 10

T35894
hypothetical protein SC9B10.25c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: T35894
R:Olliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1997
A:Reference number: Z21592
A:Accession: T35894
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-393 <OLI>
A:Cross-references: EMBL:AL009204; PIDN:CAA15815.1; GSPDB:GN00070; SCOEDB:SC9B10.25c
A:Experimental source: strain A3(2)
C:Genetics:
C:Gene: SCOEDB:SC9B10.25c
C:Superfamily: tetracycline resistance protein

Query Match 46.6%; Score 48; DB 2; Length 393;
Best Local Similarity 50.0%; Pred. No. 3.8;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 GSLPQKSHGRTQDENP 18
||:|:|:|:|:|:|
Db 373 GTVEQTHGRTQDERP 389

RESULT 11

S41043
ruml protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change 29-Oct-1999
C:Accession: S41043
R:Moreno, S.; Nurse, P.
Nature 367, 236-242, 1994
A:Title: Regulation of progression through the G1 phase of the cell cycle by the ruml protein.
A:Reference number: S41043; MUID:94166876
A:Accession: S41043
A:Molecule type: DNA
A:Residues: 1-230 <MOR>
A:Cross-references: EMBL:X77730; NID:g456668; PIDN:CAA54786.1; PID:g456669
C:Genetics:
A:Gene: ruml
A:Map position: 2
C:Superfamily: Schizosaccharomyces ruml protein

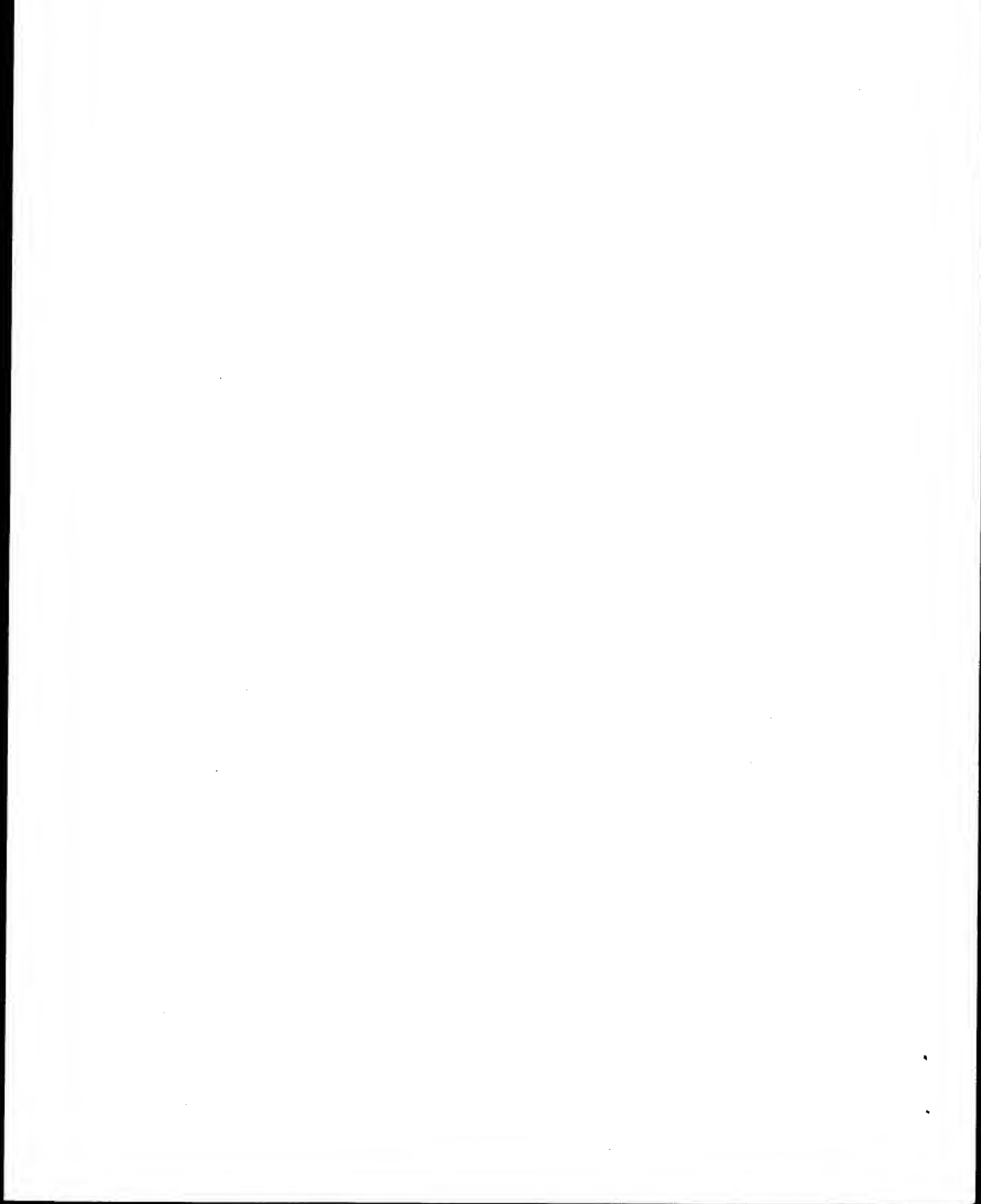
Query Match 44.7%; Score 46; DB 2; Length 230;
Best Local Similarity 64.3%; Pred. No. 4.5;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 SLPQKSHGRTQDEN 17
|:|:|:|:|:|:|
Db 211 SSFQKSRSTKRDEN 224

RESULT 12

T40233
Rumlp - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe

;Status: preliminary



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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:41:44 ; Search time 16.25 Seconds
(without alignments)
42.889 Million cell updates/sec

Title: US-09-813-383-1-copy_8_25

Perfect score: 103

Sequence: 1 HYGSLPKSHGRTQDENP 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|---------------------|
| 1 | 103 | 100.0 | 304 | 1 | P02686 homo sapien |
| 2 | 92.5 | 89.8 | 250 | 1 | P04370 mus musculus |
| 3 | 85 | 82.5 | 171 | 1 | P06906 pan troglod |
| 4 | 83.5 | 81.1 | 171 | 1 | P81558 sus scrofa |
| 5 | 79 | 76.7 | 168 | 1 | P25274 oryctolagus |
| 6 | 78.5 | 76.2 | 194 | 1 | P02688 rattus norv |
| 7 | 75.5 | 73.3 | 169 | 1 | P02687 bos taurus |
| 8 | 74.5 | 72.3 | 167 | 1 | P25188 cavia porce |
| 9 | 63.5 | 61.7 | 173 | 1 | P15720 gallus gall |
| 10 | 46 | 44.7 | 230 | 1 | P40380 schizosacch |
| 11 | 45 | 43.7 | 175 | 1 | P87346 xenopus lae |
| 12 | 45 | 43.7 | 238 | 1 | P44444 haemophilus |
| 13 | 44 | 42.7 | 497 | 1 | P08157 emericella |
| 14 | 43 | 41.7 | 497 | 1 | P41751 aspergillus |
| 15 | 43 | 41.7 | 602 | 1 | P94876 lactococcus |
| 16 | 42 | 40.8 | 491 | 1 | P06154 bos taurus |
| 17 | 42 | 40.8 | 546 | 1 | P12950 zea mays (m |
| 18 | 41 | 39.8 | 168 | 1 | P12950 zea mays (m |
| 19 | 41 | 39.8 | 647 | 1 | P12950 zea mays (m |
| 20 | 41 | 39.8 | 932 | 1 | P09897 schizosacch |
| 21 | 41 | 39.8 | 1180 | 1 | P08394 escherichia |
| 22 | 40.5 | 39.3 | 676 | 1 | P09897 xenopus lae |
| 23 | 40 | 38.8 | 187 | 1 | P19506 simian immu |
| 24 | 40 | 38.8 | 214 | 1 | P11005 xenopus lae |
| 25 | 40 | 38.8 | 477 | 1 | P09507 beet wester |
| 26 | 40 | 38.8 | 586 | 1 | P31054 coxiella bu |
| 27 | 40 | 38.8 | 587 | 1 | P04616 rhodococcus |
| 28 | 39.5 | 38.3 | 506 | 1 | P54682 dictyostell |
| 29 | 39.5 | 38.3 | 850 | 1 | P12548 aspergillus |
| 30 | 39 | 37.9 | 120 | 1 | P28757 oryza sativ |
| 31 | 39 | 37.9 | 151 | 1 | P05903 simian immu |
| 32 | 39 | 37.9 | 214 | 1 | P05903 simian immu |
| 33 | 39 | 37.9 | 231 | 1 | P02688 oryctolagus |

| | | | | | |
|----|------|------|------|---|------------|
| 34 | 39 | 37.9 | 333 | 1 | ILVC_STRAW |
| 35 | 39 | 37.9 | 434 | 1 | UL43_HSV11 |
| 36 | 39 | 37.9 | 655 | 1 | ILFL_HUMAN |
| 37 | 39 | 37.9 | 660 | 1 | AMY_BACSU |
| 38 | 39 | 37.9 | 677 | 1 | SG1_HUMAN |
| 39 | 39 | 37.9 | 954 | 1 | M3KA_HUMAN |
| 40 | 39 | 37.9 | 1136 | 1 | POLG_OMV |
| 41 | 39 | 37.9 | 1227 | 1 | PR16_HUMAN |
| 42 | 39 | 37.9 | 1256 | 1 | FTNC_CHICK |
| 43 | 39 | 37.9 | 1267 | 1 | Y211_HUMAN |
| 44 | 38.5 | 37.4 | 151 | 1 | SOD4_MAIZE |
| 45 | 38.5 | 37.4 | 151 | 1 | SOD5_MAIZE |

ALIGNMENTS

RESULT 1

| | | | | |
|----|--|-----------|------|---------|
| ID | MBP_HUMAN | STANDARD: | PRT: | 304 AA. |
| AC | P02686; Q15337; Q15338; Q15339; Q15340; | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 01-MAR-2002 (Rel. 41, Last annotation update) | | | |
| DE | Myelin basic protein (MBP) (Myelin A1 protein) (Myelin membrane | | | |
| DE | encephalitogenic protein). | | | |
| GN | MBP. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID:9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). | | | |
| RC | TISSUE=Brain; | | | |
| RX | MEDLINE=94068468; PubMed=7504278; | | | |
| RA | Pribyl T.M., Campagnoni C.W., Kampf K., Kashima T., Handley V.W., | | | |
| RA | McMahon J., Campagnoni A.T.; | | | |
| RT | "The human myelin basic protein gene is included within a 179-kilobase | | | |
| RT | transcription unit: expression in the immune and central nervous | | | |
| RT | systems." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 90:10695-10699(1993). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 3; 4; 5 AND 6). | | | |
| RC | TISSUE=Embryonic spinal cord; | | | |
| RX | MEDLINE=87311781; PubMed=2442403; | | | |
| RA | Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F., | | | |
| RA | Campagnoni A.T.; | | | |
| RT | "Evidence for the expression of four myelin basic protein variants in | | | |
| RT | the developing human spinal cord through cDNA cloning." | | | |
| RL | J. Neurosci. Res. 17:321-328(1987). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORM 6). | | | |
| RC | TISSUE=Embryonic spinal cord; | | | |
| RX | MEDLINE=86308101; PubMed=2427738; | | | |
| RA | Roth H.J., Kronquist K.E., Pretorius P.J., Crandall B.F., | | | |
| RA | Campagnoni A.T.; | | | |
| RT | "Isolation and characterization of a cDNA coding for a novel human | | | |
| RT | 17.3K myelin basic protein (MBP) variant." | | | |
| RL | J. Neurosci. Res. 16:227-238(1986). | | | |
| RN | [4] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 3 AND 5). | | | |
| RX | MEDLINE=86259714; PubMed=2425357; | | | |
| RA | Kamholz J., de Ferris F., Puckett C., Lazzarini R.A.; | | | |
| RA | "Identification of three forms of human myelin basic protein by cDNA | | | |
| RT | cloning." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986). | | | |
| RN | [5] | | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS 3; 4; 5 AND 6). | | | |
| RX | MEDLINE=89302693; PubMed=2472816; | | | |
| RA | Streicher R., Scofield W.; | | | |
| RT | "The organization of the human myelin basic protein gene. Comparison | | | |
| RT | with the mouse gene." | | | |
| RL | Biol. Chem. Hoppe-Seyler 370:503-510(1989). | | | |

| | |
|--------|-------------|
| Q59818 | streptomyce |
| P10227 | herpes simp |
| Q01167 | homo sapien |
| P00691 | bacillus su |
| P05060 | homo sapien |
| Q02779 | homo sapien |
| P20234 | o genome po |
| Q92620 | homo sapien |
| P11722 | gallus gall |
| Q92610 | homo sapien |
| P23345 | zea mays (m |
| P23346 | zea mays (m |

RP [16] SEQUENCE FROM N.A. (ISOFORM 5).
RP TISSUE=Melanoma;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [17]
RP SEQUENCE (ISOFORM 5).
RX MEDLINE=72066400; PubMed=4108501;
RA Carnegie P.R.;
RT "Amino acid sequence of the encephalitogenic basic protein from human
myelin.";
RL Biochem. J. 123:57-67(1971).
RN [18]
RP SEQUENCE OF 135-192 FROM N.A.
RX MEDLINE=90152679; PubMed=1689270;
RA Boylan K.B., Ayres T.M., Popko B., Takahashi N., Hood L.E.,
Rusiner S.B.;
RT "Repetitive DNA (TGGA)n 5' to the human myelin basic protein gene: a
new form of oligonucleotide repetitive sequence showing length
polymorphism.";
RL Genomics 6:16-22(1990).
RN [19]
RP SEQUENCE OF 179-222 (ISOFORM 5), AND REVISIONS.
RA Shapiro R., McNeally S.S., Chou F., Kibler R.F.;
RT "Encephalitogenic fragment of myelin basic protein. Amino acid
sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
RL J. Biol. Chem. 246:4630-4640(1971).
RN [10]
RP SEQUENCE OF 135-178 AND 224-304 (ISOFORM 3), AND MASS SPECTROMETRY.
RX MEDLINE=86280476; PubMed=2426402;
RA Scoble H.A., Whitaker J.N., Blemann K.;
RT "Analysis of the primary sequence of human myelin basic protein
peptides 1-44 and 90-170 by fast atom bombardment mass spectrometry.";
RL J. Neurochem. 47:614-616(1986).
RN [11]
RP SEQUENCE OF 148-304 (ISOFORM 5), AND CITRULLINATION OF C8.
RX TISSUE=Brain;
RC MEDLINE=89174797; PubMed=2466844;
RA Wood D.D., Moscarello M.A.;
RT "The isolation, characterization, and lipid-aggregating properties of
a citrulline containing myelin basic protein.";
RL J. Biol. Chem. 264:5121-5127(1989).
RN [12]
RP SEQUENCE OF 179-223 (ISOFORM 5), AND MASS SPECTROMETRY.
RX MEDLINE=84185608; PubMed=6201481;
RA Gibson B.W., Gilliom R.D., Whitaker J.N., Blemann K.;
RT "Amino acid sequence of human myelin basic protein peptide 45-89 as
determined by mass spectrometry.";
RL J. Biol. Chem. 259:5028-5031(1984).
RN [13]
RP SEQUENCE OF 246-269 (ISOFORM 3), AND ENCEPHALITOGIC PEPTIDE.
RX MEDLINE=71088405; PubMed=4099924;
RA Lennon V.A., Wilks A.V., Carnegie P.R.;
RT "Immunologic properties of the main encephalitogenic peptide from the
basic protein of human myelin.";
RL J. Immunol. 105:1223-1230(1970).
RN [14]
RP SEQUENCE OF 156-172 AND 302-304, AND CHARACTERIZATION OF C8.
RX TISSUE=Brain;
RC MEDLINE=96004793; PubMed=7574672;
RA Boulias C., Pang H., Mastronardi F., Moscarello M.A.;
RT "The isolation and characterization of four myelin basic proteins from
the unbound fraction during CM52 chromatography.";
RL Arch. Biochem. Biophys. 322:174-182(1995).
RN [15]
RP METHYLATION
RX MEDLINE=72066401; PubMed=5128665;
RA Baldwin G.S., Carnegie P.R.;
RT "Isolation and partial characterization of methylated arginines from
the encephalitogenic basic protein of myelin.";
RL Biochem. J. 123:69-74(1971).
RN [16]
RP STRUCTURE OF 135-148 BY NMR.
RX MEDLINE=95377296; PubMed=7544282;
RA Mendz G.L., Barden J.A., Martenson R.E.;
RT "Conformation of a tetradecapeptide epitope of myelin basic protein.";
RL Eur. J. Biochem. 231:659-666(1995).
RN [17]
RP 3D-STRUCTURE MODELING OF 135-279 (ISOFORM 5).
RX MEDLINE=97172499; PubMed=9020143;
RA Ridsdale R.A., Beniac D.R., Tompkins T.A., Moscarello M.A., Harauz G.;
RT "Three-dimensional structure of myelin basic protein. II. Molecular
modeling and considerations of predicted structures in multiple
sclerosis.";
RL J. Biol. Chem. 272:4269-4275(1997).
RN [18]
RP FUNCTION: The classic group of MBP isoforms (isoforms 4-14) are
with PLP the most abundant protein components of the myelin
membrane in the CNS. They have a role in both its formation and
stabilization. The smaller isoforms might have an important role
in remyelination of denuded axons in multiple sclerosis. The non-
classic group of MBP isoforms (isoforms 1-3/Golli-MBP) may
preferentially have a role in the early developing brain long
before myelination, maybe as components of transcriptional
complexes, and may also be involved in signaling pathways in T-
cells and neural cells. Differential splicing events combined to
optional posttranslational modifications give a wide spectrum of
isoforms, each of them having maybe a specialized function.
RN [19]
RP SUBUNIT: Homodimer (By similarity).
RX SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
RN [20]
RP ALTERNATIVE PRODUCTS: At least 6 isoforms; 1/Golli-MBP/HOG7
(shown here), 2/Golli-MBP2/HOG5, 3/MBP1/21.5 kDa, 4/MBP2/20.2 kDa,
5/MBP3/18.5 kDa and 6/MBP4/17.2 kDa; are produced by alternative
splicing.
RN [21]
RP TISSUE SPECIFICITY: MBP isoforms are found in both the central and
the peripheral nervous system, whereas Golli-MBP isoforms are
expressed in fetal thymus, spleen and spinal cord, as well as in
cell lines derived from the immune system.
RN [22]
RP DEVELOPMENTAL STAGE: Expression turns on abruptly in fetus of 14
embryogenesis, some of these persisting in the adult. Expression
of MBP2 is more evident at 16 weeks and its relative
proportion declined thereafter.
RN [23]
RP PTM: Several charge isoforms of MBP; C1 (the most cationic, least
modified, and most abundant form), C2, C3, C4, C5, C6, C7, C8-A
and C8-B (the less cationic form); are produced as a result of
optional PTM, such as phosphorylation, deamidation of glutamine or
asparagine, arginine citrullination and methylation. C8-A and C8-B
contain each two mass isoforms termed C8-A(H), C8-A(L), C8-B(H)
and C8-B(L), (H) standing for higher and (L) for lower molecular
weight. C3, C4 and C5 are phosphorylated. The ratio of methylated
arginine residues decreases in aging, making the protein more
cationic.
RN [24]
RP DISEASE: The reduction in the surface charge of citrullinated
and/or methylated MBP could result in a weakened attachment to the
myelin membrane. This mechanism could be operative in
demyelinating diseases such as chronic multiple sclerosis (MS),
and fulminating MS (Warburg's disease).
RN [25]
RP SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
RN [26]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
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RN [27]
RP EMBL; L18866; AAA72011.1;
DR EMBL; L18865; AAA72010.1;
DR EMBL; L18864; AAA72009.1;
DR EMBL; L18862; AAA72008.1;
DR EMBL; M30516; AAA59563.1;
DR EMBL; M30515; AAA59564.1;
DR EMBL; M30047; AAA59559.1;
DR EMBL; M13577; AAA59562.1;
DR EMBL; M20009; AAA59561.1;

Query Match 100.0%; Score 103; DB 1; Length 304;
 Best Local Similarity 100.0%; Pred. NO. 4.1e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTOENP 18
 DQ 202 HYGSLPQKSHGRTOENP 219

RESULT

MBP_MOUSE 2
 ID MBP_MOUSE STANDARD; PRT: 250 AA.
 AC P04370; Q03139; Q01585; Q03176; Q9QWP1; Q99KE4; Q61836; Q61837;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Myelin basic protein (MBP) (Myelin AI protein).
 GN MBP OR SHI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC STRAIN=C57BL/6; TISSUE=brain;
 RX MEDLINE=93186801; PubMed=7680345;
 RA Campagnoni A.T., Pribyl T.M., Campagnoni C.W., Kampf K.,
 RA Amur-Umarjee S., Landry C.F., Handley V.W., Newman S., Garbay B.,
 RA Kitamura K.;
 RT "Structure and developmental regulation of Golli-mbp, a 105-kilobase
 RT gene that encompasses the myelin basic protein gene and is expressed
 RT in cells in the oligodendrocyte lineage in the brain.";
 RL J. Biol. Chem. 268:4930-4936(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Bone marrow;
 RX MEDLINE=93057537; PubMed=1279125;
 RA Grima B., Zelenika D., Pessac B.;
 RT "A novel transcript overlapping the myelin basic protein gene.";
 RL J. Neurochem. 59:2318-2323(1992).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5; 6 AND 8).
 RX MEDLINE=86079555; PubMed=2416470;
 RA de Ferra F., Eng H., Hudson L., Kamholz J., Puckett C., Molineaux S.,
 RA Lazzarini R.A.;
 RT "Alternative splicing accounts for the four forms of myelin basic
 RT protein.";
 RL Cell 43:721-727(1985).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 5).
 RX MEDLINE=85254913; PubMed=2410136;
 RA Takahashi N., Roach A., Teplow D.B., Prusiner S.B., Hood L.E.;
 RT "Cloning and characterization of the myelin basic protein gene from
 RT mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate
 RT use of exons.";
 RL Cell 42:139-148(1985).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 6), AND SEQUENCE OF 9-194 FROM N.A.
 RP (ISOFORM 7).
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=87118269; PubMed=2433693;
 RA Newman S., Kitamura K., Campagnoni A.T.;
 RT "Identification of a cDNA coding for a fifth form of myelin basic
 RT protein in mouse.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 8).
 RC STRAIN=C57BL/6J; TISSUE=cerebellum;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

SAITO T., OKAZAKI Y., GOJOBORE T., BONO H., KASUKAWA T., SAITO R.,
 KADOTA K., MATSUDA H.A., ASHBURNER M., BATALOV S., CASAVANT T.,
 FLEISCHMANN W., GAASTERLAND T., GISSI C., KING B., KOCHIWA H.,
 KUEHL P., LEWIS S., MASUO Y., MIKALDO I., PESOLE G., QUACKENBUSH J.,
 RA SCHRIEL L.M., STAUBLI F., SUZUKI R., TOMITA M., WAGNER L., WASHIO T.,
 RA SAKAI K., OKIDO T., FURUNO M., AONO H., BALDARELLI R., BARSH G.,
 RA BLAKE K., BOFFELLI D., BOJUNGA N., CARNINCI P., DE BONALDO M.F.,
 RA BROWNSTEIN M.J., BULT C., FLETCHER C., FUJITA M., GARIBOLDI M.,
 RA GUSTINCICH S., HILL D., HOFMANN M., HUME D.A., KAMIYA M., LEE N.H.,
 RA LYONS P., MARCHIONNI L., MASHIMA J., MAZZARELLI J., MOMBERTS P.,
 RA NORDONE P., KING B., RINGWALD M., RODRIGUEZ I., SAKAMOTO N.,
 RA SASAKI H., SATO K., SCHOENBACH C., SEYA T., SHIBATA Y., STORCH K.-F.,
 RA SUZUKI H., TOYO-OKA K., WANG K.H., WEITZ C., WHITTAKER C., WILMING L.,
 RA WYNSHAW-BORIS A., YOSHIDA K., HASEGAWA Y., KAWAJI H., KOHESUKI S.,
 RA HAYASHIZAKI Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690(2001).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 9).
 RC TISSUE=Breast tumor;
 RA Straussberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 135-157 FROM N.A.
 RX MEDLINE=89252919; PubMed=2470651;
 RA Miura M., Tamura T.A., Aoyama A., Mikoshiba K.;
 RT "The promoter elements of the mouse myelin basic protein gene
 RT function efficiently in NG108-15 neuronal/glial cells.";
 RL Gene 75:31-38(1989).
 RN [9]
 RP PARTIAL SEQUENCE FROM N.A. (25 AA INSERTION OF ISOFORMS 4; 6 AND 9).
 RX MEDLINE=86259714; PubMed=2425357;
 RA Kamholz J., de Ferra F., Puckett C., Lazzarini R.A.;
 RT "Identification of three forms of human myelin basic protein by cDNA
 RT cloning.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).
 RN [10]
 RP SEQUENCE OF 193-222 FROM N.A.
 RX MEDLINE=84119431; PubMed=6198644;
 RA Zeller N.K., Hunkeler M.J., Campagnoni A.T., Sprague J.,
 RA Lazzarini R.A.;
 RT "Characterization of mouse myelin basic protein messenger RNAs with a
 RT myelin basic protein cDNA clone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:18-22(1984).
 RN [11]
 RP PARTIAL SEQUENCE FROM N.A. (22 AA INSERTION OF ISOFORMS 10 AND 11).
 RX TISSUE=Spinal cord;
 RX MEDLINE=91162193; PubMed=1705957;
 RA Aruga J., Okano H., Mikoshiba K.;
 RT "Identification of the new isoforms of mouse myelin basic protein: the
 RT existence of exon 5a.";
 RL J. Neurochem. 56:1222-1226(1991).
 RN [12]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 12; 13 AND 14).
 RX MEDLINE=93203993; PubMed=7681106;
 RA Nakajima K., Ikenaka K., Kagawa T., Aruga J., Nakao J., Nakahira K.,
 RA Shiota C., Kim S.U., Mikoshiba K.;
 RT "Novel isoforms of mouse myelin basic protein predominantly expressed
 RT in embryonic stage.";
 RL J. Neurochem. 60:1554-1563(1993).
 RN [13]
 RP SEQUENCE OF 191-224 FROM N.A.
 RX MEDLINE=88196094; PubMed=2452084;
 RA Okano H., Tamura T., Miura M., Aoyama A., Ikenaka K., Oshimura M.,
 RA Mikoshiba K.;
 RT "Gene organization and transcription of duplicated MBP genes of myelin
 RT deficient (shi(mld)) mutant mouse.";
 RL EMBO J. 7:77-83(1988).
 RN [14]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=98409779; PubMed=9736652;
 RA Landry C.F., Pribyl T.M., Ellison J.A., Givogri M.I., Kampf K.,
 RA Campagnoni C.W., Campagnoni A.T.;

FT MOD_RES 56 56 PHOSPHORYLATION.
 FT MOD_RES 96 96 PHOSPHORYLATION.
 FT MOD_RES 101 101 DEAMINATION (PARTIAL) (PROBABLE).
 FT MOD_RES 105 105 METHYLATION (MONO- OR DI-).
 FT MOD_RES 113 113 PHOSPHORYLATION.
 FT MOD_RES 128 128 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 145 145 DEAMINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 157 157 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 159 159 PHOSPHORYLATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 163 163 PHOSPHORYLATION.
 FT MOD_RES 168 168 CITRULLINATION (BY SIMILARITY).
 FT CONFLICT 46 46 S -> G (IN REF. 2).
 SQ SEQUENCE 168 AA; 18217 MW; EC3C97ACD2C08EA6 CRC64;

Query Match 76.7%; Score 79; DB 1; Length 168;
 Best Local Similarity 83.3%; Pred. No. 2.5e-06;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRQDENP 18
 IIIIIIIIII I IIIII
 DB 66 HYGSLPQKSHGRQDENP 83

RESULT 6
 MBP_RAT
 ID MBP_RAT STANDARD; PRT; 194 AA.
 AC P02688; Q921J4; Q921J5; Q921J6;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Myelin basic protein S (MBP S).
 GN MBP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
 RA Lobell A.M., Wigzell H.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RX MEDLINE=87026249; PubMed=2429678;
 RA Schach M., Budzinski R.M., Stoffel W.;
 RT "Cloned proteolipid protein and myelin basic protein cDNA.
 Transcription of the two genes during myelination.";
 RL Biol. Chem. Hoppe-Seyler 367:825-834(1986).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RX MEDLINE=84026484; PubMed=6194889;
 RA Roach A., Boylan K.B., Horvath S., Prusiner S.B., Hood L.E.;
 RT "Characterization of cloned cDNA representing rat myelin basic
 protein: absence of expression in brain of shiverer mutant mice.";
 RL Cell 34:799-806(1983).
 RN [4]
 RP SEQUENCE (ISOFORM 4).
 RX MEDLINE=75127359; PubMed=4141893;
 RA Dunkley P.R., Carnegie P.R.;
 RT "Amino acid sequence of the smaller basic protein from rat brain
 myelin.";
 RL Biochem. J. 141:243-255(1974).
 RN [5]
 RP SEQUENCE OF 130-194 FROM N.A.
 RX STRAIN=Lewis; TISSUE=Brain;
 RL MEDLINE=96078224; PubMed=7578863;
 RA Nalotka J., Doramair K.;
 RT "Alternative splicing and cDNA sequence of myelin basic protein gene
 of the Lewis rat.";
 RL Autoimmunity 20:67-68(1995).
 RN [6]
 RP SEQUENCE OF 45-111 (ISOFORM 4).

RX MEDLINE=73180720; PubMed=4122324;
 RA McFarlin D.E., Blank S.E., Kibler R.F., McKneally S.S., Shapiro R.;
 RT "Experimental allergic encephalomyelitis in the rat: response to
 encephalitogenic proteins and peptides.";
 RL Science 179:478-480(1973).
 CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the
 myelin membrane in the CNS. Has a role in both the formation and
 stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 function in the assembly of an optimized, biochemically functional
 myelin membrane (by similarity).
 CC -!- SUBUNIT: Homodimer (by similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -!- ALTERNATIVE PRODUCTS: At least 4 isoforms; 1/21.5 kDa (shown
 here), 2/18.5 kDa, 3/17 kDa and 4/14 kDa; are produced by
 alternative splicing.
 CC -!- TISSUE SPECIFICITY: Found in both the central and the peripheral
 nervous system.
 CC -!- PTM: As in other animals, several charge isomers may be produced
 as a result of optional posttranslational modifications, such as
 phosphorylation of serine or threonine residues, deamidation of
 glutamine or asparagine residues, citrullination and methylation
 of arginine residues.
 CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC
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 or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AJ132895; CAAL0804.1; -;
 CC EMBL; AJ132896; CAAL0805.1; -;
 CC EMBL; AJ132897; CAAL0806.1; -;
 CC EMBL; AJ132898; CAAL0807.1; -;
 CC EMBL; M25889; AAA41575.1; -;
 CC EMBL; K00512; -; NOT_ANNOTATED_CDS.
 CC EMBL; X72392; -; NOT_ANNOTATED_CDS.
 CC PIR; A03142; MBRTS.
 CC PIR; B24351; B24351.
 CC PIR; A21062; A21062.
 CC HSSP; P02686; LOCL.
 CC InterPro: IPR000548; Myelin_BP.
 CC Pfam: PF01669; Myelin_MBP; 1.
 CC PRINTS; PR00212; MYELINMBP.
 CC PROSITE; PS00569; MYELIN_MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Citrullination; Autoimmune encephalomyelitis; Alternative splicing.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT MOD_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY
 SIMILARITY).
 FT MOD_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 56 56 PHOSPHORYLATION (PARTIAL) (BY
 SIMILARITY).
 FT MOD_RES 121 121 PHOSPHORYLATION (PARTIAL) (BY
 SIMILARITY).
 FT MOD_RES 126 126 DEAMINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 130 130 METHYLATION (MONO-:44% OR DI-:11%).
 FT MOD_RES 138 138 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 153 153 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 171 171 DEAMINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 183 183 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 185 185 PHOSPHORYLATION (PARTIAL) (BY
 SIMILARITY).
 FT MOD_RES 189 189 PHOSPHORYLATION (PARTIAL) (BY
 SIMILARITY).
 FT MOD_RES 194 194 CITRULLINATION (BY SIMILARITY).
 FT VARSPLIC 59 84 MISSING (IN ISOFORM 2 AND ISOFORM 4).
 FT VARSPLIC 140 180 MISSING (IN ISOFORM 3 AND ISOFORM 4).

FT CONFLICT 46 47 SG -> GS (IN REF. 6).
 FT CONFLICT 191 191 M -> I (IN REF. 1 AND 3).
 SQ SEQUENCE 194 AA; 21371 MW; 68FB399C250B4C50 CRC64;

Query Match 76.2%; Score 78.5; DB 1; Length 194;
 Best Local Similarity 88.9%; Pred. No. 3.6e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 HYGSLPQKSHGRTQDENP 18
 ||||||| |||||
 DB 92 HYGSLPQKSO-RTQDENP 108

RESULT 7

MEP_BOVIN STANDARD; PRT; 169 AA.
 ID MEP_BOVIN
 AC P02687; Q9TSA6; Q9TSG3; O9BGM8;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa microtubule
 stabilizing protein).
 GN MBP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72007306; PubMed=5096093;
 RA Eylar E.H., Brostoff S.W., Hashim G., Caccam J., Burnett P.;
 RT "Basic A1 protein of the myelin membrane. The complete amino acid
 sequence.";
 RL J. Biol. Chem. 246:5770-5784(1971).
 RN [2]
 RP REVISION.
 RX MEDLINE=74070688; PubMed=4129204;
 RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;
 RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";
 RL J. Biol. Chem. 249:559-567(1974).
 RN [3]
 RP SEQUENCE OF 4-56 FROM N.A.
 RA Pietrowski D., Medugorac I., Foerster M.;
 RT "A new MBP allele in Bos taurus is characterized by BseNI PCR-RFLP.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 43-87.
 RA Shapira R., McKenally S.S., Chou F.C.-H., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640(1971).
 RN [5]
 RP SEQUENCE OF 38-58 AND 119-141.
 RC TISSUE=Brain;
 RX MEDLINE=93003019; PubMed=1382581;
 RA Pirollet F., Derancourt J., Halech J., Job D., Margolis R.L.;
 RT "Ca(2+)-calmodulin regulated effectors of microtubule stability in
 bovine brain.";
 RL Biochemistry 31:8849-8855(1992).
 RN [6]
 RP SEQUENCE OF 30-42; 74-89 AND 114-129.
 RX MEDLINE=96107211; PubMed=8530487;
 RA Prasad K., Barouch W., Martin B.M., Greene L.E., Eisenberg E.;
 RT "Purification of a new clathrin assembly protein from bovine brain
 coated vesicles and its identification as myelin basic protein.";
 RL J. Biol. Chem. 270:30551-30556(1995).
 RN [7]
 RP SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.
 RX MEDLINE=70178977; PubMed=5442707;
 RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;
 RT "Experimental allergic encephalomyelitis: synthesis of

RT disease-inducing site of the basic protein.";
 RL Science 168:1220-1223(1970).
 RN [8]
 RP METHYLATION.
 RX MEDLINE=71153946; PubMed=4994464;
 RA Brostoff S.W., Eylar E.H.;
 RT "Localization of methylated arginine in the A1 protein from myelin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).
 RN [9]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=76167591; PubMed=57115;
 RA Chou F.C.-H., Chou C.-H.J., Shapira R., Kibler R.F.;
 RT "Basis of microheterogeneity of myelin basic protein.";
 RL J. Biol. Chem. 251:2671-2679(1976).
 RN [10]
 RP SEQUENCE OF 97-104, AND PHOSPHORYLATION OF THR-97.
 RX MEDLINE=91060584; PubMed=1700979;
 RA Erickson A.K., Payne D.M., Martino P.A., Rossomando A.J.,
 RA Shabanowitz J., Weber M.J., Hunt D.F., Sturgill T.W.;
 RT "Identification by mass spectrometry of threonine 97 in bovine myelin
 basic protein as a specific phosphorylation site for mitogen-activated
 protein kinase.";
 RL J. Biol. Chem. 265:19728-19735(1990).
 RN [11]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=98153125; PubMed=9485392;
 RA Zand R., Li M.X., Jin X., Lubman D.;
 RT "Determination of the sites of posttranslational modifications in the
 charge isomers of bovine myelin basic protein by capillary
 electrophoresis-mass spectroscopy.";
 RL Biochemistry 37:2441-2449(1998).
 RN [12]
 RP DIMERIZATION.
 RX MEDLINE=80198320; PubMed=6155143;
 RA Smith R.;
 RT "Sedimentation analysis of the self-association of bovine myelin basic
 protein.";
 RL Biochemistry 19:1826-1831(1980).
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
 myelin membrane in the CNS. Has a role in both the formation and
 stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 function in the assembly of an optimized, biochemically functional
 myelin membrane (By similarity).
 CC -1- SUBUNIT: Homodimer; self-associates in the presence of lysolipid.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral
 nervous system.
 CC -1- PTM: At least 6 charge isomers; C1 (the most cationic and least
 modified form), C2, C3, C4, C5 AND C6 (the less cationic form);
 CC are produced as a result of optional posttranslational
 CC modifications, such as phosphorylation of serine or threonine
 CC residues, deamidation of glutamine or asparagine residues,
 CC citrullination and methylation of arginine residues.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC
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 CC
 CC EMBL; AF222693; AAK00645.1;
 CC PIR; A03140; MBBOB.
 CC HSP; P02686; LOCL.
 CC InterPro: IPR000548; Myelin_BP.
 CC Pfam: PF01669; Myelin_MBP.1.
 CC PRINTS; PR00212; MYELINBP.
 CC PROSITE; PS00569; MYELIN_MBP; 1.
 CC Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;
 CC Citrullination; Autoimmune encephalomyelitis.
 KW

FT DOMAIN 43 87 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS (EAE) 1.
 FT DOMAIN 114 122 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS (EAE) 2.
 FT MOD_RES 1 1 ACETYLATION
 FT MOD_RES 7 7 PHOSPHORYLATION (IN C5 AND C6).
 FT MOD_RES 23 23 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 29 29 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 54 54 PHOSPHORYLATION (IN C4, C5 AND C6).
 FT MOD_RES 97 97 PHOSPHORYLATION (BY MAPK) (IN C3, C4, C5 AND C6).
 FT MOD_RES 102 102 DEAMIDATION (IN C5).
 FT MOD_RES 106 106 METHYLATION (MONO- OR DI-).
 FT MOD_RES 114 114 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 129 129 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 146 146 DEAMIDATION (IN C2).
 FT MOD_RES 158 158 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 160 160 PHOSPHORYLATION (IN C4 AND C6).
 FT MOD_RES 164 164 PHOSPHORYLATION (IN C3, C5 AND C6).
 FT MOD_RES 169 169 CITRULLINATION (PROBABLE).
 SQ SEQUENCE 169 AA; 18323 MW; 8E1157B7A1978484 CRC64;

Query Match 73.3%; Score 75.5; DB 1; Length 169;
 Best Local Similarity 78.9%; Pred. No. 1e-05;
 Matches 15; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHG-RTQDENP 18
 |||||: | | ||||
 Db 66 HYGSLPQKSHG-RTQDENP 84

RESULT 8

ID MBP-CAVPO STANDARD; PRT; 167 AA.
 AC P25188;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-2002 (Rel. 41, Last annotation update)
 DE Myelin basic protein (MBP).
 GN MBP.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=84215086; PubMed=6202840;
 RA Deibler G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;
 RT "Sequence of guinea pig myelin basic protein.";
 RL J. Neurochem. 43:100-105(1984).
 RN [2]
 RP SEQUENCE OF 7-156 FROM N.A.
 RC STRAIN-Hartley; TISSUE-Spinal cord;
 RA Kim G., Tanuma N., Matsumoto Y.;
 RT "DNA vaccination using Guinea pig myelin basic protein coding region
 in experimental autoimmune encephalomyelitis.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 45-87.
 RA Shapira R., McNeally S.S., Chou F., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640(1971).
 RN [4]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=76025020; PubMed=51849;
 RA Deibler G.E., Martenson R.E., Kramer A.J., Kies M.W.;
 RT "The contribution of phosphorylation and loss of COOH-terminal
 arginine to the microheterogeneity of myelin basic protein.";
 RL J. Biol. Chem. 250:7931-7938(1975).
 CC -I- FUNCTION: Is, with PLP, the most abundant protein component of the
 myelin membrane in the CNS. Has a role in both the formation and

CC stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 CC function in the assembly of an optimized, biochemically functional
 CC myelin membrane (By similarity).
 CC -I- SUBUNIT: Homodimer (By similarity).
 CC -I- TISSUE SPECIFICITY: Cytoplasmic side of myelin.
 CC -I- TISSUE SPECIFICITY: Found in both the central and the peripheral
 CC nervous system.
 CC -I- PTM: At least 5 charge isomers; C1 (the most cationic, least
 CC modified, and most abundant form), C2, C3, C4 and C5 (the less
 CC cationic form); are produced as a result of optional
 CC posttranslational modifications such as phosphorylation of serine
 CC or threonine residues, deamidation of glutamine or asparagine
 CC residues, citrullination and methylation of arginine residues. C1
 CC and C2 are unphosphorylated, C3 and C4 are monophosphorylated and
 CC C5 is phosphorylated at two positions.
 CC -I- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC
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DR EMBL; AF074337; AAC26130.1; -
 DR PIR; A37246; A37246.
 DR PIR; C92087; C92087.
 DR HSSP; P02686; IQCL.
 DR InterPro; IPR000548; Myelin_BP.
 DR Pfam; PF01669; Myelin_MBP; 1.
 DR PRINTS; PR00212; MYELINBP.
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Citrullination; Autoimmune encephalomyelitis.
 FT DOMAIN 45 87 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS (EAE) 1.
 FT DOMAIN 114 122 INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS (EAE) 2.
 FT MOD_RES 1 1 ACETYLATION.
 FT MOD_RES 7 7 PHOSPHORYLATION (PARTIAL) (BY
 FT SIMILARITY).
 FT MOD_RES 25 25 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 31 31 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 56 56 PHOSPHORYLATION (PARTIAL) (BY
 FT SIMILARITY).
 FT MOD_RES 97 97 PHOSPHORYLATION (PARTIAL) (BY
 FT SIMILARITY).
 FT MOD_RES 102 102 DEAMIDATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 106 106 METHYLATION (MONO-OR DI-) (BY
 FT SIMILARITY).
 FT MOD_RES 114 114 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 129 129 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 144 144 DEAMIDATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 156 156 CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT MOD_RES 158 158 PHOSPHORYLATION (PARTIAL) (BY
 FT SIMILARITY).
 FT MOD_RES 162 162 PHOSPHORYLATION (PARTIAL) (BY
 FT SIMILARITY).
 FT MOD_RES 167 167 CITRULLINATION (BY SIMILARITY).
 SQ SEQUENCE 167 AA; 18213 MW; 866D31F1E5ACFEA6 CRC64;

Query Match 72.3%; Score 74.5; DB 1; Length 167;
 Best Local Similarity 83.3%; Pred. No. 1.5e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGSLPQKSHGRTQDENP 18
 |||||: | | ||||
 Db 68 HYGSLPQKSHGRTQDENP 84


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RESULT 11
ID MBP_XENLA STANDARD; PRT; 175 AA.
AC P87346;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myelin basic protein (MBP) (Myelin A1 protein).
GN MBP.
OS xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J; TISSUE=Brain;
RA Nagata S., Ogino K.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Have a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -!- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as
CC phosphorylation of serine or threonine residues, deamidation of
CC glutamine or asparagine residues, citrullination and methylation
CC of arginine residues.
CC -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC
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CC
CC EMBL; AB000736; BAA19174.1; -.
CC HSP; P02686; IOLC.
CC InterPro; IPR000548; Myelin_BP.
CC Pfam; PF01669; Myelin_MBP.1.
CC PRINTS; PR00212; MYELINBP.
CC Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
CC Citrullination.
CC INIT_MET 0 0 BY SIMILARITY.
CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
CC MOD_RES 6 6 PHOSPHORYLATION (PARTIAL) (BY
CC SIMILARITY).
CC MOD_RES 24 24 CITRULLINATION (PARTIAL) (BY SIMILARITY).
CC MOD_RES 32 32 CITRULLINATION (PARTIAL) (BY SIMILARITY).
CC MOD_RES 57 57 PHOSPHORYLATION (PARTIAL) (BY
CC SIMILARITY).
CC MOD_RES 96 96 DEAMIDATION (PARTIAL) (BY SIMILARITY).
CC MOD_RES 102 102 PHOSPHORYLATION (PARTIAL) (BY
CC SIMILARITY).
CC MOD_RES 107 107 METHYLATION (MONO-OR DI-) (BY
CC SIMILARITY).
CC MOD_RES 110 110 SIMILARITY).
CC MOD_RES 116 116 PHOSPHORYLATION (BY SIMILARITY).
CC MOD_RES 166 166 PHOSPHORYLATION (PARTIAL) (BY
CC SIMILARITY).
CC MOD_RES 170 170 PHOSPHORYLATION (PARTIAL) (BY
CC SIMILARITY).
CC MOD_RES 175 175 CITRULLINATION (BY SIMILARITY).
CC SEQUENCE 175 AA; 19589 MW; FE89A119CFBC2A9 CRC64;

Query Match 43.7%; Score 45; DB 1; Length 175;
Best Local Similarity 45.5%; Pred. No. 1.6;
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

QY 1 HYGSLPOKS---HGRTQDENP 18
Db 68 YLSSSPQSPYHAHGRHVDNDP 89

RESULT 12
ID RNPH_HAEIN STANDARD; PRT; 238 AA.
AC P44444;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease PH (EC 2.7.7.56) (RNase PH) (TRNA
DE nucleotidyltransferase).
DE RPH OR HI0273.
GN Haemophilus influenzae.
OS Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd."
RL Science 269:496-512(1995).
CC -!- FUNCTION: RNase PH is a PHOSPHORYLYTIC EXORIBONUCLEASE THAT
CC REMOVES NUCLEOTIDE RESIDUES FOLLOWING THE -CCA TERMINUS OF TRNA
CC AND ADDS NUCLEOTIDES TO THE ENDS OF RNA MOLECULES BY USING
CC NUCLEOSIDE DIPHOSPHATES AS SUBSTRATES (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: [trna](N+1) + phosphate = [trna](N) + a
CC nucleoside diphosphate.
CC -!- SIMILARITY: BELONGS TO THE RNASE PH FAMILY.
CC
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CC
CC EMBL; U3713; AAC21939.1; -.
CC TIGR; HI0273; -.
CC InterPro; IPR001247; 3_ExoRNase.
CC Pfam; PF01138; RNase_PH; 1.
CC PROSITE; PS01277; RIBONUCLEASE_PH; 1.
CC TRANSFERASE; Nucleotidyltransferase; trna processing;
CC Complete proteome.
CC SEQUENCE 238 AA; 25789 MW; B67015EBF8FBA23F CRC64;

Query Match 43.7%; Score 45; DB 1; Length 238;
Best Local Similarity 53.3%; Pred. No. 2.3;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 YGSLPQKSHGRTODE 16
Db 63 YGMLPRSTHSMQRE 77

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RESULT 13
DHALL_EMENI STANDARD; PRT; 497 AA.
AC P08157;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aldehyde dehydrogenase (EC 1.2.1.3) (ALDDH).
GN ALDA OR ASPA.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=5072;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87248080; PubMed=3036652;
RA Pickett M., Gwynne D.I., Buxton F.P., Elliott R., Davies R.W.,
RA Lockington R.A., Scazzocchio C., Sealy-Lewis H.M.;
RT "Cloning and characterization of the alda gene of Aspergillus
RT nidulans.";
RL Gene 51:217-226(1987).
CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC -1- PATHWAY: SECOND STEP IN ETHANOL UTILIZATION.
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC -----
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CC -----
CC EMBL; M16197; AAA3293.1; -.
CC HSP; P05091; ICW3.
CC InterPro: IPR002086; Aldehyde_dehydr.
CC Pfam: PF00171; aldedh; 1.
CC PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
CC PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Oxidoreductase; NAD.
FT NP_BIND 241 246 NAD (ADP PART) (BY SIMILARITY).
FT ACT_SITE 264 264 BY SIMILARITY.
FT ACT_SITE 298 298 BY SIMILARITY.
SQ SEQUENCE 497 AA; 54088 MW; 1711FCEA993E571B CRC64;

Query Match 42.7%; Score 44; DB 1; Length 497;
Best Local Similarity 44.4%; Pred. No. 7.8;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLFQKSHGRTQDENP 18
DB 127 YYAGWADKINGQITDNP 144
: | | | | | | |
: | | | | | | |

RESULT 14
DHALL_ASPIG STANDARD; PRT; 497 AA.
AC P41751;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aldehyde dehydrogenase (EC 1.2.1.3) (ALDDH).
GN ALDA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90108706; PubMed=2606357;
RA O'Connell M.J., Kelly J.M.;
RA "Physical characterization of the aldehyde-dehydrogenase-encoding
RA gene of Aspergillus niger.";
RL Gene 84:173-180(1989).
CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC -1- PATHWAY: SECOND STEP IN ETHANOL UTILIZATION.
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC -----
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CC -----
CC EMBL; M32351; AAA87596.1; -.
CC HSP; P05091; ICW3.
CC InterPro: IPR002086; Aldehyde_dehydr.
CC Pfam: PF00171; aldedh; 1.
CC PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
CC PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Oxidoreductase; NAD.
FT NP_BIND 242 247 NAD (ADP PART) (BY SIMILARITY).
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 299 299 BY SIMILARITY.
SQ SEQUENCE 497 AA; 53809 MW; 47CA353FFD8A50E8 CRC64;

Query Match 41.7%; Score 43; DB 1; Length 497;
Best Local Similarity 47.1%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 HYGSLFQKSHGRTQDEN 17
DB 128 YYGWADKINGQITDNP 144
: | | | | | | |
: | | | | | | |

RESULT 15
PEF2_LACLC STANDARD; PRT; 602 AA.
ID PEF2_LACLC STANDARD; PRT; 602 AA.
AC P94876;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oligoendopeptidase F, chromosomal (EC 3.4.24.-).
GN PEPF2.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCDO 763;
RX MEDLINE=97352670; PubMed=9209029;
RA Nardi M., Renault P., Monnet V.;
RT "Duplication of the pepF gene and shuffling of DNA fragments on the
RT lactose plasmid of Lactococcus lactis.";
RL J. Bacteriol. 179:4164-4171(1997).
CC -1- FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO
CC ACIDS WITH A RATHER WIDE SPECIFICITY.
CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
CC -----
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 16:41:23 ; Search time 41.39 Seconds
(without alignments)
75.233 Million cell updates/sec

Title: US-09-813-383-1-copy_8_25
Perfect score: 103
Sequence: 1 HYGSLPKSHGRTQDENP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhmc.*
8: sp_ordanelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 50 | 48.5 | 238 | 2 Q9AES0 | Q9AES0 pasteurella |
| 2 | 48 | 46.6 | 393 | 2 O50532 | O50532 streptomyc |
| 3 | 47.5 | 46.1 | 1123 | 10 Q9LH08 | Q9LH08 arabidopsi |
| 4 | 47 | 45.6 | 235 | 2 Q9X528 | Q9X528 legionella |
| 5 | 46 | 44.7 | 257 | 16 Q9KVD6 | Q9KVD6 vibrio chol |
| 6 | 46 | 44.7 | 632 | 16 Q9I250 | Q9I250 pseudomonas |
| 7 | 45 | 43.7 | 238 | 16 Q9CJW5 | Q9CJW5 pasteurella |
| 8 | 45 | 43.7 | 301 | 10 Q9ZQW9 | Q9ZQW9 oryza sativ |
| 9 | 44 | 42.7 | 257 | 17 Q97UP0 | Q97UP0 sulfolobus |
| 10 | 44 | 42.7 | 497 | 3 Q9C1Q6 | Q9C1Q6 emericella |
| 11 | 44 | 42.7 | 497 | 3 Q9C1Q5 | Q9C1Q5 emericella |
| 12 | 44 | 42.7 | 497 | 3 Q9C1Q4 | Q9C1Q4 emericella |
| 13 | 44 | 42.7 | 914 | 4 Q99493 | Q99493 homo sapien |
| 14 | 44 | 42.7 | 1260 | 5 Q9V468 | Q9V468 drosophila |
| 15 | 44 | 42.7 | 1312 | 4 Q99700 | Q99700 homo sapien |
| 16 | 43.5 | 42.2 | 124 | 2 Q9F273 | Q9F273 actinobacill |

| | | | | | |
|----|------|------|------|-----------|--------------------|
| 17 | 43 | 41.7 | 366 | 5 Q96AC6 | Q96AC6 musca domes |
| 18 | 43 | 41.7 | 516 | 4 Q9P290 | Q9P290 homo sapien |
| 19 | 43 | 41.7 | 625 | 2 Q9R9E7 | Q9R9E7 pseudomonas |
| 20 | 43 | 41.7 | 1100 | 5 Q9VUE7 | Q9VUE7 drosophila |
| 21 | 42 | 40.8 | 241 | 16 Q9PD74 | Q9PD74 xylella fas |
| 22 | 42 | 40.8 | 316 | 16 Q9HYU2 | Q9HYU2 pseudomonas |
| 23 | 42 | 40.8 | 333 | 16 Q9CLF9 | Q9CLF9 pasteurella |
| 24 | 42 | 40.8 | 353 | 5 Q9NBJ2 | Q9NBJ2 drosophila |
| 25 | 42 | 40.8 | 364 | 10 Q9SMD5 | Q9SMD5 lycopersico |
| 26 | 42 | 40.8 | 366 | 5 Q9NBJ3 | Q9NBJ3 drosophila |
| 27 | 42 | 40.8 | 377 | 2 Q9ZAN3 | Q9ZAN3 vibrio angu |
| 28 | 42 | 40.8 | 578 | 5 Q97281 | Q97281 plasmodium |
| 29 | 42 | 40.8 | 684 | 4 Q9HCM6 | Q9HCM6 homo sapien |
| 30 | 42 | 40.8 | 733 | 11 Q922V1 | Q922V1 mus musculu |
| 31 | 42 | 40.8 | 738 | 11 Q91255 | Q91255 mus musculu |
| 32 | 42 | 40.8 | 842 | 2 Q93JF4 | Q93JF4 streptomyc |
| 33 | 42 | 40.8 | 955 | 4 Q9Y2M1 | Q9Y2M1 homo sapien |
| 34 | 42 | 40.8 | 1743 | 3 Q9C3Z2 | Q9C3Z2 cochllobolu |
| 35 | 42 | 40.8 | 1865 | 4 Q14185 | Q14185 homo sapien |
| 36 | 42 | 40.8 | 2531 | 5 Q16004 | Q16004 lytechinus |
| 37 | 41.5 | 40.3 | 94 | 5 Q61684 | Q61684 drosophila |
| 38 | 41.5 | 40.3 | 134 | 4 Q96NR2 | Q96NR2 homo sapien |
| 39 | 41 | 39.8 | 115 | 5 Q23174 | Q23174 caenorhabdi |
| 40 | 41 | 39.8 | 205 | 16 Q9A5D9 | Q9A5D9 caulobacter |
| 41 | 41 | 39.8 | 254 | 16 Q9PHE8 | Q9PHE8 xylella fas |
| 42 | 41 | 39.8 | 264 | 5 Q9GTX5 | Q9GTX5 plasmodium |
| 43 | 41 | 39.8 | 278 | 3 Q9GTX5 | Q9GTX5 plasmodium |
| 44 | 41 | 39.8 | 280 | 5 Q2743 | Q2743 plasmodium |
| 45 | 41 | 39.8 | 280 | 5 Q25852 | Q25852 plasmodium |

ALIGNMENTS

| | | | | | |
|---|--------------|------|---------|--|--|
| RESULT 1 | | | | | |
| Q9AES0 | PRELIMINARY; | PRT: | 238 AA. | | |
| ID Q9AES0 | | | | | |
| AC Q9AES0; | | | | | |
| DT 01-JUN-2001 (TrEMBLrel. 17, Created) | | | | | |
| DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) | | | | | |
| DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update) | | | | | |
| DE RIBONUCLEASE PH-LIKE PROTEIN. | | | | | |
| OS Pasteurella haemolytica. | | | | | |
| OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; | | | | | |
| OC Mannheimia. | | | | | |
| OX NCBI_TaxID=75985; | | | | | |
| RN [1] | | | | | |
| RP SEQUENCE FROM N.A. | | | | | |
| RA LO R.Y., Graham M.R.; | | | | | |
| RT "Putative TonB dependent receptor of Mannheimia haemolytica."; | | | | | |
| RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases. | | | | | |
| DR EMBL: A1028475; AAK29744.1; - | | | | | |
| DR InterPro: IPR001247; 3_ExoRNase. | | | | | |
| DR InterPro: IPR002381; RNase_PH. | | | | | |
| DR Pfam: PF01138; RNase_PH; 1. | | | | | |
| DR PROSITE: PS01277; RIBONUCLEASE_PH; 1. | | | | | |
| SQ SEQUENCE 238 AA; 25893 MW; EF0BE4382716BD2F CRC64; | | | | | |

Query Match 48.5%; Score 50; DB 2; Length 238;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YGSLPKSHGRTQDE 16
|||: |||
Db 63 YGMLPRATHSRQRE 77

RESULT 2
O50532
1D O50532
AC O50532
DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DI 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE HYPOTHETICAL 41.1 KDA PROTEIN.
 GN SC9B10.25C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OX Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN NCBI_TaxID=1902;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parkhill J., Barrell B.G., Rastandream M.A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Redenbach M., Kleser H.M., Denapaita D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; AL009204; CAA15815.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 393 AA; 41113 MW; 880B301145BB5FA6 CRC64;

Query Match 46.6%; Score 48; DB 2; Length 393;
 Best Local Similarity 50.0%; Pred. No. 5.5;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 GSLPQKSHGRQTQDENP 18
 I::I::I::I::I::I

DB 373 GTVEQHTGERQDERP 388

RESULT 3

ID Q9LH08 PRELIMINARY; PRT; 1123 AA.
 AC Q9LH08;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE COPIA-TYPE POL POLYPROTEIN-LIKE.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eutrosids II; Brassicales; Brassicaceae; Arabidopsis.
 RN NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Nakamura Y.;
 RT "Structural Analysis of Arabidopsis thaliana Chromosome 3. III."
 DR EMBL; AP002459; BAA97087.1; -.
 DR InterPro; IPR001969; Asp-Protease.
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00665; rve; 2.
 DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
 KW Polyprotein.
 SQ SEQUENCE 1123 AA; 127169 MW; 8C5B6319E3B12022 CRC64;

Query Match 46.1%; Score 47.5; DB 10; Length 1123;
 Best Local Similarity 55.6%; Pred. No. 23;
 Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 4 SLPOKSHGR--TQDENP 18
 I::I::I::I::I::I

DB 508 SNPQKHGRPVGSKDKNP 525

RESULT 4

ID Q9X528 PRELIMINARY; PRT; 235 AA.
 AC Q9X528;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DI 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE RIBONUCLEASE PH.
 GN RPH.
 OS Legionella pneumophila.
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
 OC Legionellaceae; Legionella.
 RN NCBI_TaxID=446;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=130B;
 RA Kim S.J., Choe Y.K.;
 RT "Cloning and sequencing of the rph gene encoding RNase PH from
 Legionella pneumophila."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF120720; AAD28218.1; -.
 DR InterPro; IPR001247; 3-EXONase.
 DR InterPro; IPR002381; RNase_PH.
 DR Pfam; PF01138; RNase_PH; 1.
 DR PROSITE; PS01277; RIBONUCLEASE_PH; 1.
 SQ SEQUENCE 235 AA; 26110 MW; B139F9AE430050CE CRC64;

Query Match 45.6%; Score 47; DB 2; Length 235;
 Best Local Similarity 53.3%; Pred. No. 4.5;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YGSLPQKSHGRQTQDE 16
 I::I::I::I::I::I

DB 63 YGMLPRATHSRTERE 77

RESULT 5

ID Q9KVD6 PRELIMINARY; PRT; 257 AA.
 AC Q9KVD6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE RIBONUCLEASE PH.
 GN VC0210.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 RN NCBI_TaxID=666;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.C., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae."
 RL Nature 406:477-483(2000).
 DR EMBL; AE004111; AAF93386.1; -.
 DR TIGR; VC0210;
 DR InterPro; IPR001247; 3-EXONase.
 DR InterPro; IPR002381; RNase_PH.
 DR Pfam; PF01138; RNase_PH; 1.

DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE HYPOTHETICAL PROTEIN SSO2964.
 GN SSO2964.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=2132296; PubMed=1142726;
 RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Etrauso G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE006887; AAK43068.1;
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 257 AA; 28092 MW; BC3A972C9A576AF8 CRC64;

Query Match 42.7%; Score 44; DB 17; Length 257;
 Best Local Similarity 44.4%; Pred. No. 16;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 ||||| : |||
 Db 79 HYGSLSYELHSDPDHNP 96

RESULT 10

Q9C1Q6 PRELIMINARY; PRT; 497 AA.
 AC Q9C1Q6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ALDEHYDE DEHYDROGENASE ALDH.
 GN ALDA.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21269214; PubMed=11102439;
 RA Filippi M., Mathieu M., Cirpus I., Panozzo C., Felenbok B.;
 RT "Regulation of the aldehyde dehydrogenase gene (aldA) and its role in
 the control of the co-inducer level necessary for induction of the
 ethanol utilization pathway in Aspergillus nidulans.";
 RL J. Biol. Chem. 276:6950-6958(2001).
 DR EMBL; AF260123; AAK18072.1;
 DR HSSP; P05091; ICW3.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; aldedh; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 FT VARIANT 191 E -> Q.
 FT VARIANT 208 G -> P.
 FT VARIANT 247 R -> P.
 FT VARIANT 409 E -> V.
 SO SEQUENCE 497 AA; 54138 MW; 9C6CFC62731A25BD CRC64;

Query Match 42.7%; Score 44; DB 3; Length 497;
 Best Local Similarity 44.4%; Pred. No. 36;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 :| :||| |||
 Db 127 YYAGWADKIHGTIDTNP 144

RESULT 11

Q9C1Q5 PRELIMINARY; PRT; 497 AA.
 AC Q9C1Q5;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ALDEHYDE DEHYDROGENASE ALDH15.
 GN ALDA.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21269214; PubMed=11102439;
 RA Filippi M., Mathieu M., Cirpus I., Panozzo C., Felenbok B.;
 RT "Regulation of the aldehyde dehydrogenase gene (aldA) and its role in
 the control of the co-inducer level necessary for induction of the
 ethanol utilization pathway in Aspergillus nidulans.";
 RL J. Biol. Chem. 276:6950-6958(2001).
 DR EMBL; AF260124; AAK18073.1;
 DR HSSP; P05091; ICW3.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; aldedh; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 FT VARIANT 286 V -> A.
 SO SEQUENCE 497 AA; 54166 MW; 65849D1DCA94A5F5 CRC64;

Query Match 42.7%; Score 44; DB 3; Length 497;
 Best Local Similarity 44.4%; Pred. No. 36;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 HYGSLPQKSHGRTQDENP 18
 :| :||| |||
 Db 127 YYAGWADKIHGTIDTNP 144

RESULT 12

Q9C1Q4 PRELIMINARY; PRT; 497 AA.
 AC Q9C1Q4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ALDEHYDE DEHYDROGENASE ALDH57.
 GN ALDA.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=5072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21269214; PubMed=11102439;
 RA Filippi M., Mathieu M., Cirpus I., Panozzo C., Felenbok B.;
 RT "Regulation of the aldehyde dehydrogenase gene (aldA) and its role in
 the control of the co-inducer level necessary for induction of the
 ethanol utilization pathway in Aspergillus nidulans.";
 RL J. Biol. Chem. 276:6950-6958(2001).
 DR EMBL; AF260125; AAK18074.1;
 DR HSSP; P05091; ICW3.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; aldedh; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 FT VARIANT 338 S -> G.

RA Sahba S.;
RT "Moderate expansion of a normally biallelic trinucleotide repeat in
RL spinocerebellar ataxia type 2.";
RL Nat. Genet. 14:269-276(1996).
DR EMBL: U70323; AAB19200.1; -.
SQ SEQUENCE 1312 AA; 140140 MW; CF6E358C14A83AF5 CRC64;

Query Match 42.7%; Score 44; DB 4; Length 1312;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSLPQKSHGRTQDENP 18
||:|:| | | | |
Db 521 GSMPSRSTSTHTSDENP 536

Search completed: August 28, 2002, 16:41:25
Job time: 377 sec